A STUDY ON STABILITY OF YIELD AND YIELD CONTRIBUTING CHARACTERS IN INDIAN MUSTARD [*Brassica juncea* (L.) Czern & Coss]

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By:

RAGHUNATH SINGH YADAV

Research Centre:

Deptt. of Genetics & Plant Breeding
Brahmanand Mahavidyalaya Rath,
Hamirpur (U.P.)
And Nehru Mahavidyalaya,
Lalitpur (U.P.)

Supervised By:

Dr. S.P. Singh
Reader & Head,
Deptt. of Genetics & Plant Breeding
Brahmanand Mahavidyalaya, Rath,
Hamirpur (U.P.)

Dedicated
To my
Venerable
Parents

Dr. S.P. Singh
M.Sc.(Ag.), Ph.D.

Reader & Head.
Department of Genetics &
Plant Breeding
B.N.V/D/C. Rath
Hamirpur, (U.P).

CERTIFICATE

It gives immense pleasure to certify the thesis entitled **"A Study on Stability of Yield and Yield Contributing Characters in Indian Mustard" [*Brassica juncea* (L.) Czern & Coss]** submitted to the Bundelkhand University, Jhansi for award to degree of Doctor of Philosophy in Genetics & Plant Breeding, is a record of bonafide research work.

Carried out by Sri Raghunath Singh Yadav, under my supervision. Thesis embodies the work of candidate himself and is fit for population. He had put the required attendance in the department during this period as per ordinance of B.N.V/D/C. Rath Hamirpur(U.P.). The present thesis has been completed within specified and prescribed time. I wish the candidate all the success.

Place : Rath
Date : 26.01.09

(Dr.S.P.Singh)

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RAGHUNATH SINGH YADAV

CONTENT

Introduction

Chapter-I

INTRODUCTION

India is one of the major oilseed producing country in the world. Among oilseed crops, Brassica group of oilseeds, commonly known as rape seed and mustard, account for over 13.2 per cent of the world's edible oil supply and are the third most important edible oil source after soybean and palm. The global scenario of rapeseed & mustard showed that during 1996-97, its area was 5324.2 million hectare and production was 35.10 million tonnes with the productivity of 1451 kg/ha. Among the 7 Asian countries, China and India together account for 95.4 per cent of the total hectarage and 96.7 per cent of the rapeseed-mustard production in Asia. The yield level ranged from 466 (Kazakhstan) to 1889 kg/ha (Korea Republic) (FAO production year book, 1997). In India rapeseed and mustard occupies second position in acreage with 4.8 million hectare after groundnut (7.0mha.). The contribution of rapeseed and mustard was 7.01 million tonnes and production 4.71 million tonnes with productivity of 667kg/ha. Northern states of the country are the major rapeseed and mustard producing regions accounting for about 90 per cent of country's total production. Rajasthan ranking first with 32.5 per cent of country's total rapeseed and mustard production followed by U.P., Gujarat, Haryana, M.P. and Assam

(Appedix-1) The oil extracted from rapeseed and mustard is used for culinary purposes and the meal cake, The residue after the oil extraction, as cattle feed. In addition to this, the seeds are used as spices as components in preparation of salad juices curries and pickles. Besides, there is heavy industrial demand of the oil for lubricant and toilet perposes. Rape and mustard seed have about 40 per cent oil on dry weight basis. The meal contains 38-44 per cent high quality protein.

The area production and productivity of mustard in U.P. during last five years given in table (A).

Year	Total Area in Lakh ha.	Total production in lakh.me.tan.	Productivity in Qu/ha.
2002-03	5.60	5.02	8.96
2003-04	5.36	5.34	9.95
2004-05	6.19	6.14	9.92
2005-06	5.62	6.46	11.49
2006-07	5.99	6.12	10.22

Source:- Rabi faslan ki saghan paddhatiyan 2007-2008. Directorali of Ag. U.P.

Nevertheless, the quantity of oil available in the country is far short of the need of the people. The per capita availability of edible

oil in India is only 18g/day as against the normal requirement of 30g/day. To meet the country's requirement of edible oil India has to spend a huge money every year on imports of edible oil. Further more, production and productivity of oilseeds in the country have virtually remained stagnant over the year. The average yield of this crop in the country is 848 kg/ha.

Among Brassica group of oilseed crops Indian mustard or Rai [B. juncea (L.) Czern & Coss] occupies quite a large acreage of total rape seed and mustard growing area of Northern India. It has almost replaced yellow sarson on account of its greater resistance to aphids, drought condition and shattering. (Pawlowski.1970, Ray.1978). Due to its economic importance and major growing crop especially in Northern India, Indian mustard requires special attention for its improvement.

Prime consideration with the improvement of this crop is its yield of seeds/ha. But yield is a complex character, governed by several genes interacting each other. Greatly influenced by environmental conditions and is the result of interaction of the environment and the genotype. It is therefore, the genetic diversity present in a crop plays an important rote in improvement of the crop. Greater the diversity more is the genetic potentiality and wider is the scope for improvement. It is therefore, paramount importance for a plant breeder to study as large collection of genotypes /varieties

as possible. Variability in crop plants provides an opportunity for selecting desirable types.

As, yield is a very complex character it is difficult to study and its improvement is even more difficult. Emphasis cannot be laid upon the yield alone due to its complexity in inheritance and being influenced by the environmental factors. A practical if not an ideal approach would then appear to study yield character by breaking it down into its components and studying each one separately as well as in combination with one another. Whitehouse, Thompson and Rioberio (1958) and Grafius (1959) have suggested implicity or explicity there may not be gene for yield per se but rather for the various components the multiplicative interaction of which results in the artifice of yield. Therefore a essential of have some information on the association between different yield components and their relative contribution to yield. A knowledge of such relation ships essential if selection for the simultaneous improvement of yield components and in turn yield is to be effective. In this context the correlation studies assume special importance as it tell us about the genetic association of different characters with seed yield. But correlation measures do not employ any cause and effect relationship path coefficient analysis as. suggested by Wright (1921) on the other hand gives a clear picture cause and effect as it slice off the correlation in to the estimates of direct and indirect contribution of each character towards, yield.

Heritability which is an index of transmissibility of characters from parents to offspring is a suitable measure for assessing the magnitude of genetic portion of total variability. Due consideration must there fore be given to heritability estimates of the characters while improvement in a crop by selection for various characters is to be made. But heritability alone does not give true picture of genetic improvement likely to be made during selection in subsequent generations, it is the genetic gain which predicts the speed of genetic improvement to be affected by selecting a particular portion of the population. Therefore fore crop improvement by selection. It is essential to study the extent of heritability along with genetic advance.

The effects of genotype and environment as phenotype may not be always independent. The phenotypic response to charge in environment is not same for all genotypes, the consequences of variation in phenotypic depend up on the environment. Since GxE interaction has marking effect on genotypic (Comstock and Moll, 1963) hence these interactions are of considerable importance to plant breeders in identifying the genotypes suitable for favourable location/environment or even different fertility levels and assumes importance for potential expression of characters under interest. The main efforts of geneticists are to reduce them or to scale the out. The genotypes adjusting their phenotypic state in response to the environment so that they are able to give their maximum yield or

near maximum economic returns are called "well buffered" genotype (Allard and Hansche 1964). The Indian mustard is generally sown in marginal or sub-marginal lands under poor fertility condition. The low responsiveness to fertilizers in Indian mustard is a limiting factor for poor yield, susceptibility of various genotypes to different insect pest (aphids) and diseases are an other limitation to get self sufficiency in yellow revolution. Hence present investigation was carried out utilizing 25 genotypes over diverse environments to assess to the stability of seed yield and its component traits in Indian mustard under different dates of sowing with varying fertility levels and locations.

The main objective of present investigation is given as under:-

1. To assess the amount and nature of genotype environment interaction.

2. To evaluate and screen out the potential genotypes giving consistant performance and genotypes giving good performance under specific environment of Bunkelkhand.

3. To select the genotypes on the basis of stability parameters for various characters.

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Review of literature

Review of literature

Chapter-II

REVIEW OF LITERATURE

1. Genetics variability and heritability:

Chandola *et al.* (1973) observed in *B. Juncea* that plant height showed high value of genetic advance. However, low genetic advance with low heritability value was expressed by yield per plant.

Srivastava and Das (1973) studied genetic parameter and correlation coefficient in *Brassica campestris* Var. sarson (Pram) and found that seed yield per plant posses high genotypic coefficient of variation. High heritability in broad sense was associated with high genetic advance for number of siliquae on main shoot and for seed yield per plant.

Tiwari and Singh (1973) observed moderately high heritability percentage in narrow sense for yield per plant (45.77%) and plant height (42.27%) in Brassica *juncea.*

Thurling (1974) observed high heritability for flowering period, seeds per pod, seed weight and yield in variety span. Majority of characters had higher heritabilities.

Katiyar *et al.* (1976) reported in Indian mustard that the heritability and genetic advance were high for plant height and seed yield per plant. Heritability for number of branches was also food to be high.

Paul (1978) observed that heritability in broad sense was moderate to high in *Brassica juncea*. The mean genotypic coefficient of variation was highest for seed size (92.78%).

Li and Guan (1981) studied heritability and variability in *napus.* They reported average heritability value for branching position, plant height, length of main inflorescence in eight varieties to be 91.6, 88.8 and 82.0 per cent, respectively. The heritability values for yield components were low. The coefficient of genetic variation for number of siliqua per plant and number of effective branches were comparatively high, while those for number of seeds per siliqua and 1000-seed weight were relatively low.

Yadav (1983) worked out coefficient of variability, heritability, correlation coefficient and path analysis in brown sarson (*B. campestris*) and reported that, secondary branches had greatest phenotypic and genotypic coefficient of variability. Heritability estimates were high for total number of siliqua per plant, all other characters had medium to low heritability.

Chen *et al.* (1983) studied heritability and path analysis in rage, they reported that, heritability was very low for seed yield.

Olivieri and Parrini (1983) reported in rapeseed, relatively high heritability for 1000-seed weight and low for sil1qua per plant.

Yadav *et al.* (1985) studied genetic variability in brown sarson comprising 39 genotypes which showed significant variability for all the characters studied particularly for plant height, number of siliqua per plant, number of siliqua on main shoot, number of secondary branches and seed yield. There was very good agreement between genotypic coefficient of variability and phenotypic coefficient of variability for all characters. Heritability estimates ranged from medium to high.

Bang *et al.* (1986) studied heritability of some agronomic characters in mustard and found that the heritability estimates in broad sense were high for flowering time (0.992) and seed yield (0.987) and moderately high for plant height, raceme length and total number of branches.

Singh *et al* (1987) recorded low to medium heritability in number of primary branches and seed per siliqua.

Li *et al.* (1990) studied heritability of 24 characters in 60 genotypes of *Brassica napus*. They grouped these characters into 3 groups viz., yield (19 characters), morphological and oil composition characters. All these groups showed low heritability estimates.

***Kumar at al.* (1994)** recorded data on 12 yield components in 15 genotypes of *Brassica Juncea*, 3 of *B. napus*, 3 of *B. napus,* 4 of *B. chinensis* grown during rabi 1985-86. High level of genetic advance

and heritability in broad sense were 'noted in several characters yield improvement was thought possible through selection for yield per plant, harvest index, siliquae per plant, number of secondary branches and 1000-seed weight.

2. **Correlation Coefficient:**

Kunn and Kim (1977) worked out correlation and path coefficient in rape they observed non significant correlation between yield and earliness both at genotypic and phenotypic level. Path analysis revealed that lateness had a direct effect on yield.

Rawat and Anand (1977) studied the association of seed yield with its components characters in Indian mustard and reported that yield was correlated with number of primary branches number of secondary branches, plant height, number of seeds per slliqua, and thousand seed weight. They further reported that maximum contribution to yield was through the primary branches and secondary branches.

Pathak and Tripathi (1978) reported appositive and non significant association of test weight with seed yield.

Pauw and Baker (1978) investigated the character association in four traits of *Brassica campestris* and reported that only height and days to maturity were appreciably correlated.

Yadav *et al.* (1978) studied correlation in Indian mustard and reported that number of days to on set of flowering was negatively correlated with number of days to 50 per cent flowering, 1000-seed weight and number of days to maturity, while number of days to 50 per cent flowering was positively correlated with 100o-seed weight and number of days to maturity. A positive correlation was found between number of days to maturity and 1000-seed weight.

Prasad *et al.* (1979) studied correlation coefficient in *Brassies cornpestris* Var. sarson (Prain) and reported that grain yield was found significantly associated with plant height. number of primary and secondary branches, length of main siliqua bearing branch, number of siliqua on main axis, number of siliqua per plant, days to maturity, grains per siliqua and 1000-grain weight.

Tak and Salroo (1979) studied association of yield and yield components in *Brassica compestris* (L.) and reported that seed yield per plant was positively correlated with period of flowering, pods per plant, plant height, 500-seed weight and days to maturity.

Srivastava *et al.*, (1983) studied correlation in *Brassica juncea* (L.) and concluded that the seed yield was positively associated with number of primary branches, secondary branches, plant height and days to maturity.

Uddin *et al.* (1983) worked out correlation for yield and some quantitative characters in Indian mustard. They concluded that seed yield was found to be positively and significantly correlated with plant height, primary and secondary branches and seeds per pod at phenotypic level. However, at genotypic level yield per plant showed significant and negative correlations with all above characters except plant height. Most of the correlations were positive at phenotypic level but negative at genotypic level.

Yadav (1983) found that seed yield was correlated with number of primary branches, number of siliqua per plant, number of inflorescence, 1000-seed weight and plants height.

Singh *et al.* (1985) investigated morpho-physiological attributes in relation to seed yield in Indian mustard and found that total siliqua number per plant, number of secondary branches per plant and 1000-seed weight were significantly and positively correlated with seed yield.

Chaudhary *et al.* (1987) studied correlation of nine important characters of mustard. Study indicated that yield per plant showed positive and significant genotypic correlation with days to maturity, plant height, number of primary branches, number of siliqua on main raceme, on lateral branches and siliqua length. 1000-seed weight and number of primary branches had the highest positive correlation with yield.

Gupta *et al.* (1987) studied correction of metric traits contributing towards oil yield in Indian mustard among the 51 diverse *Brassica Juncea* genotypes. Harvest index, oil percentage and seed yield were positively correlated with oil yield at the genotypic and phenotypic level with genotypic correlation being generally higher than phenotypic ones.

Kumar *et al.* (1987) studied association of economic traits in yellow sarson. [*B. compestris* Var. yellow sarson]. Yield was most highly correlated, with number of secondary branches followed by number of primary branches, days to first and 50 percent flowering and height.

Singh *et al.* (1987) reported that seed yield was positively correlated with stem height, number of siliqua per plant, primary and secondary branches per plant in Indian mustard.

Chaturvedi *et al.* (1988) studied correlation and reported that number of primary branches secondary branches, tertiary branches and length of main receme showed positive correlation with yield.

Kumar *et al.* (1988) studied correlation coefficient analysis in Indian mustard and found that yield was positively and significantly correlated with number of primary branches, secondary branches and num per siliqua per plant.

Chaudhary et al. (1990) evaluated Brassica genotypes for physio-morphological parameters under moisture stress condition. Simple correlation studies revealed that positive association of yield with secondary branches per plant, siliqua number per plant and biological yield. Negative association of seed yield was found with number of seeds per siliqua.

Dhillon *et al.* (1990) studied association of 7 characters in 51 lines and found that plant height had the highest direct effect on seed yield while secondary branches/plant, main raceme length and pods/main raceme were also major contributors.

Reddy (1991) studied correlation in Indian mustard (*B. Juncea* (L.) Czern and Coss) and indicated that seed yield is positively and significantly correlated with leaf area index, primary and secondary branches per plant, siliqua per plant, seeds per siliqua and plant weight of si.iqua and seeds.

Zaman *et al.* (1992) studied correlation, on swedish advanced rape lines that had been crossed with *Brassica Juncea. B. carinata* and *B. alboglabra* to incorporate earliness to enable cultivation of rape in Bangladesh. Results showed seeds per pod to be negatively correlated with pods per plant, thereby imposing limitations on simultaneous improvement of the two traits. Moreover, both traits were positively correlated with. maturity,

imposing further constraints on the selection of early and high yielding genotypes.

Chaudhary *et al.* (1994) studied correlations in yellow seeded *Brassica tournefortii* for 10 yield components in 35 genotypes. Number of siliquae per main raceme, primary branches per plant and recemes per plant more significantly and positively correlated with seed yield.

Singh *et al.* (1995) studied correlations in eight diverse cultivars for 10 characters in *B. juncea*. They reported that oil content was positively associated with 1000-seed weight and seed yield indicating the possibility of simultaneous improvement for these characters.

3. PATH ANALYSIS

Srivahare *et al.* (1975) adopted path coefficient analysis for yield in Indian mustard and concluded that number of primary and secondary branches, the number of seed per siliqua and 1000-seed weight, each has a large direct effect over yield per plant. The plant height and days to flowering affects yield via number of secondary branches.

Labana *et al.* (1977) employed path analysis for yield in Indian mustard. The analysis revealed that the secondary branches had the maximum direct effect on yield. Pods on main shoot, number

of primary branches and days to maturity showed a high direct effect, whereas, days to flowering gave a high direct negative effect. Seeds per siliqua showed a high direct negative effect via pod length and days to flowering. 1000-seed weight showed a high negative indirect effect through days to flowering but showed a positive indirect effect through days to maturity.

Singh *at al.* (1978) applied path analysis in Indian mustard and concluded' that the number of siliqua on main shoot and number of secondary branches were the main yield components.

Das *et al.* (1984) reported that strongest direct effect on yield were given by primary branches in *Brassica juncea*, siliqua number and seed per siliqua in *Brassica* compestris.

Kumar *et al.* (1987) studied correlation and path coefficients of economic traits on yield in yellow sarson and found that yield was highly correlated with number of primary branches, days to first and 50 per cent flowering. Path analysis indicated that plant height, number of primary branches, number of seed per siliqua, days to 50 percent flowering had high direct effect on yield.

Mishra *et al.* (1987) applied path analysis in yellow seeded Indian mustard, they reported that seed weight per unit volume had the greatest direct effect on yield, which was also positively affected by days to maturity, plant height, number of secondary branches,

though these positive direct effect were nullified by negative indirect effects on the seed yield. Despite of these negative indirect effect on seed yield, the traits number of primary branches, number of siliqua per plant appeared important in improving yield owing to their positive direct effect on it.

Behl *et al.* (1992) studied morphophysiological determinants of oil yield in *Brassica juncea* under dry land conditions. They reported that the greatest effects on 011 yield were directly from seed yield and indirectly from siliquae per plant, seed weight and leaf turgor pressure. Sub components of shoot length, seeds per siliqua, secondary branches, siliqua length, relative water content and osmotic potential contributed to oil yield via one or more main components.

Kandil *et al.* (1994) reported that number of pods per plant had the highest direct and indirect effect on yield plant in *B. napus* L. and was responsible for 40 per cent of the variation in this character.

Ramani *et al.* (1995) collected data on 10 yield components in Indian mustard grown under 12 different irrigation regimes which were subjected to path analysis. The number of primary branches per plant had the most direct positive effect on yield followed by number of secondary branches per plant.

Saini *et al.* (1995) studied character association and path coefficient analysis to determine relationship between growth and yield parameters in 28 lines of yellow and brown sarson (*B. compestris* Var. sarson) seed number per siliqus, harvest inde_ and 1000-seed weight. were identified as important factors affecting seed yield.

4. **Stability Parameters:**

Badwal and Labana (1989) found significant genotypes environment interaction for all characters under study. Five parents and five hybrids were shown to be stable and produced a high seed yield. Significant positive correlation was observed between seed yield and plant height primary branches, secondary branches and siliqua length which indicated that these were yield components that contributed to yield stability.

Sharma and Roy (1993) conducted an experiments on 3 dates of sowing with 14 *napus* and *juncea* genotypes and observed significant GxE interaction for both characters and crops. Both linear and non-linear components were significant for maturity where as non-linear component was significant only for seed yield. In toria, the earliest maturity genotypes, TS 29 had a stable yield and the highest yielding genotypes, M 27 was stable for maturity. In Indian mustard, Dira 367 gave above average stability for yield and maturity, TM4 was stable for maturity.

Mahto (1996) observed significant GxE (linear) interactions for all the characters except number of siliquae per plant, plant height and number of secondary branches. he evaluate stability of indivisual genotypes based on regression coefficient and deviation from regression.

Lekh-Raj *et al.* (1997) evaluated 54 selecting of gobhisarson, rape, juncea and carinata on six environment and 3 dates of sowing. The contribution of reproductive period, days to maturity and days to 50% flowering to seed yield was not stable for all the characters.

Mahto (1999) evaluated 19 genotypes of Indian mustard in three environment and observed significant GxE (linear) for all the characters except no. of siliquae/plant, plant height and number of secondary branches.

Mahto and Haider (2000) observed considerable genetic variability and significant environment and G x E interaction for all the 11 characters. Among the parents, RW 873 and Kranti proved to be the most stale genotypes for the majority of traits.

Dhillon, S.S. *et al.* (2001) studied twenty-eight genotypes of Indian mustard to find out genotype environment interaction (GxE) and phenotypic stability for grain yield and its components. Sufficient G x E interaction was exhibited by the genotypes for all the characters except oil content. However, characters differed as

regard the contribution of linear and non-linear components of G x E interaction. The genotype PBR 181, PBR 171 AND PBR 91 have stability for most of the important yield contributing characters as well as seed yield. Thus, these genotypes can be utilized to develop stable strains having wider adaptability in future breeding programmes.

Gunasekera *et al.* (2003) studied the effect of genotype and environment interaction on seed yield of mustard and canola in low rainfall area of Mediterranean type environments of South Western Australia and observed average phenotypic stability for mustard genotypes Monty across the environments. Mustard genotypes 887.1.6.1, 82NO22-98 showed general adaptability for yield across the environments genotypes JM25 and JM33 showed specific adaptation to drought and high temperature canola genotype Oscar produced lowest yield across environments and showed high sensitivity to environments.

Patel *et al.* (2005) noted significant GxE interactions and GxE (linear) for seed yield, length of main branch, branches/plant and seeds/siliquae. Genotypes SKM 2026 and NPJ 82 were found stable for siliquae/plant and oil content suggesting that these genotypes can be exploited for further breeding programme.

Gupta *et al.* (2006) studied 7 characters in Indian mustard of 10 genotypes in three years at Bikaner and observed significant GxE

interactions for all the traits. The GxE linear was significant for test weight and days to maturity.

Singh *et al.* (2006) observed considerable variability for 1000-seed weight, seed yield and other characters genotypes Vardan and Seeta were found suitable for low input environment while Krishna for input rich cultivation.

Mahto and Mahto (2007) reported significant environment and G x E interaction for all the characters studied when tested against pooled error. The pooled deviation from regression were also significant for all the characters except primary branches, but the magnitude of linear component was higher in comparision to pooled deviation indicating that major portion of interaction was linear and predication over environment was still possible.

Sigh and Kumar (2007) noted significant differences among genotypes and environments in toria. The linear component was significant for all the characters except number of primary branches suggesting that prediction of genotypes were possible across the environments. Genotype IC212033 was observed to be desirable and stable for yield and other characters.

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Material & Methods

Chapter-III

MATERIAL AND METHODS

The experimental material for present study was comprised of 25 strains/varieties of Indian mustard [*Brassica juncea* (L.) Czern and Coss.] selected on the basis of genotypic /phenotypic diversity. These lines were obtained from the gene bank maintained at Oilseeds section of C.S. Azad University of Agriculture & Technology, Kanpur-208002. The name, origin/pedigree and salient characteristics of the genotypes are listed in table 1.

All the genotypes were sown in a completely randomized block design replicated thrice in twentyfour varying environment i.e. two dates of sowing, two locations, two years and three levels of fertilizers during *rabi* 2005-06. The dates of sowing were 25^{th} September 2005 (normal) and 25^{th} October 2005 (late). The normal dose of fertilizer was 100 kg N, 60 kg P_2O_5 and 40 kg K_2O/ha while low dose was 50 kg N, 30 kg P_2O_5 and 20 kg K_2O/ha and nil fertilizers respectively. The experiment was laid out at two locations namely, Brahmanand Mahavidyalaya, Rath (Hamirpur) and Nehru Mahavidyalaya, Lalitpur Research Farms. At Lalitpur location same doses of fertilizer were used while dates of sowing were 27^{th} September

2005 as normal and 27th October 2005 as late. The same experiments were repeated next year also with same treatments

Each genotypes was sown in two rows of 5 meter long spaced at 45 x 15 cm between rows and between plants respectively at both the locations and years. All the recommended agronomical practices were adopted to raise a good crop except fertilizer doses. Which were applied as per treatments.

Recording of the data:

The observations were recorded on ten randomly selected plants from each genotypes and each replication for following characters.

(1) **Days to flower:** It was observed on plot basis in each genotype when 50 percent plants start flowering from the date of sowing in days.

(2) **Number of primary branches:** Total numbers of primary branches containing siliquae were counted at the time of harvesting in each genotype and each replication.

(3) **Number of secondary branches :** Total number of secondary branches arise from primaries were counted at the time of harvesting.

(4) **Plant height:** It was measured in cm at the time of harvesting from level of the earth to top of the plant with the help of a meter scale.

(5) **Length of main fruiting branches:** The length of main fruiting branches was measured in centimeter by the help of meter scale at the time of harvesting.

(6) **Number of siliquae on main fruiting branches:** Total number of siliquae on main fruiting branch bearing seeds were counted at the time of threshing.

(7) **1000-seed weight :** Exact 1000 seeds were counted randomly after threshing and weighed in gram up to two decimal points with the help of electronic balance.

(8) **Days to maturity:** It was recorded as day taken by genotype for its physiological maturity from date of sowing.

(9) **Yield per plant :** All the ten plants were threshed together and their seeds were weighed in gram up to two decimal points with the help of electronic balance

and the yield per plant was taken after dividing the yield by number of plants.

(10) Oil content (%): It was estimated in dry seeds using NMR instrument in percent up to two decimal points.

Statistical / biometrical analysis

Statistical analyses of the data were conducted as usual procedure while stability analyses were carried out by four models as given below:

Statistical Analysis:

The subject of statistics deals with variability and how to deal with it. In the planning and conduct of an environmental of ecological investigation, the items used to control environmental variability are (a) refinement of experimental technique, (b) selection of homogeneous material and / or environments, (c) grouping (blocking, stratifying) material into homogeneous subgroups (blocks, strata), and (d) measurement of related variables and use of covariance. Item (c) is an application of the Fisherian principle of control.

The second Fisherian principle of replication is sued to reduce further the variability of estimates. The third Fisherian principle of randomization provides for unbiased estimates of effects and their variances. There are many ways of blocking (arranging) the

experimental units (Eus) in a comparative experiment with v treatments. If the sample of Eus is from a homogeneous population, then no blocking is required and a completely randomized experiment design (ED) of the v treatments randomly allotted to the rv Eus is used. The replicate number (sample size) for each treatment is r unless unequal replication is desired. If homogeneous blocks of size v are available to accommodate all v treatments, a randomized complete block ED (all v treatments in each block, not necessarily an equal number of times) is used.

Randomized Block Design

Randomized Block Design (RBD). The stability was computed analyzing the data using Randomized Block Design. Adoption of this design is useful when the variation between the blocks is significant. The main features of this design are presented below:

1. Construct a table of totals and means.
2. Compute the entries in a ANOVA table.
3. Compute a CV.
4. Conduct significance tests.
5. Compute means and standard errors.

To illustrate the analysis suppose we have a RBD with r-blocks and p-treatments. Let y_{ij} represent the yield of the j-th treatment in the i^{th} block.

1. Construct a two-way block by treatment table and compute totals and means as shown in Table-3.4.

2. Construct ANOVA table. This takes the same general form as the ANOVA table for the CRD except that it includes and additional sou) ce of variation for blocks. The entries in Table 3.5 are obtained as follows :

   1. Source – Total variation is partitioned into components due to blocks, treatments, and error.

   2. d.f. – Degrees of freedom are one less than the number of classes in each variance.

   3. The error Degrees of freedom value is obtained by difference d.f. Error = d.f. Tot. – d.f. Rep. – d.f. Tot.

Table : Summary table of data from a randomized block

Block		Treatment			Sum	Mean
1	1	2	-	p	1+2+p	y_1
-	-	-	-	-	-	-
Sum	T^1	T^2	-	T^p	g	G

$R_1 = \Sigma \mid y_{ij}$ = total yield of i-th block

$y^i = R_i/p$ = mean of i-th block

$T_1 = \Sigma \mid y_{ij}$ = total yield of j-th block

$y^j = T_i/p$ = mean of i-th treatment

$G = \Sigma \mid R_i/p = \Sigma_j T_j$ = grant total of all

$G = G/rp$ = grand mean

Table : Analysis of variance for a randomized block design.

S. No.	Source	d.f.	S.S.	M.S.
1.	Replication	r-1	$SS_R = \frac{\sum_{j=1}^{r} (\sum_{i=1}^{g} x_{ij})^2}{g} - \frac{(\sum_{i=1}^{g} \sum_{j=1}^{r} x_{ij})^2}{rg}$	MS_R
2.	Genotype	g-1	$SS_G = \frac{\sum_{i=1}^{g} (\sum_{j=1}^{r} x_{ij})^2}{r} - \frac{(\sum_{i=1}^{g} \sum_{j=1}^{r} x_{ij})^2}{rg}$	MS_G
3.	Error	(r-1)(g-1)	$SS_E = SS_T - SS_G - SS_R$	MS_E
	Total	(rg-1)		
	Total	(rg-1)	$SS_T = \sum_{i=1}^{g} \sum_{j=1}^{r} x_{ij}^2 - \frac{(\sum_{i=1}^{g} \sum_{j=1}^{r} x_{ij})^2}{rg}$	

Where

Xij = value of ith genotype in jith replication,

r = number of replications, and

g = number of genotypes.

4. Mean squares – Divide the sums of squares by the degrees of freedom on the same line in the ANOVA.

   a. MSR = SSR /(r-1).

   b. MST = SST /(p-1).

   c. MSE = SSE /(r 1) (p-1)

   F: MSE is the divisor for all ratios

   a. F_R = MSR/MSE.

   b. F_T = MST/MSE

5. CV (coefficient of variation) : % CV = (MSE/$\bar{\bar{y}}$ Y) 100

Significance Tests: F_t, with (p-1) and (r-1) (P-1) degree of freedom is a test statistic for the hypothesis that all treatment means are equal against the alternative that at least one mean differs from the others. in other words, F_t tests the significance of the differences among treatment means. If F_r is larger than the 1% F in the table, the difference are said to be highly significant (* *). If F_t is greater than the 5% F but smaller than the 1% F the difference are significant (*). If F_t is smaller than the 5% F, the difference are not significant (NS). F_R with (r=1) and (r-1) (p-1) df, is only an approximate test statistics for differences among blocks. If F_r is greater than the F in the F table, it is an indication that blocking has been effective in reducing experimental error. There is no appropriate error term in the ANOVA of an RBD for testing the significance of block differences. F_r is not always computed because it is only approximate and, more to point, if blocking is done correctly, the differences among blocks are deliberately maximized. It seems pointless in this case to test the hypothesis that the differences among blocks are zero.

Means and Standard Errors

With the randomized block design, as with the CRD, the sample means estimate the true means of the treatments. We have

$\mu_i = \bar{Y}_i = T_i/r$, similarly, with this ANOVA, as in the ANOVA for the CRD, MSE = s^2 is an estimate of the variance per plot (variation among plots treated alike). It is used in the computation of standard errors and in the construction of interval estimates.

$$S_{\bar{y}} = \sqrt{2MSE/r}$$

Since, r is the same for all treatments, s_y is he same for all. The $1-\alpha$) 100% confidence interval estimate of a treatment mean, L (μ_J), is $L(\mu_j) = (y_j) \pm t_\alpha \sqrt{2MSE/r}$ where t_α is the two-tailed, α-level t-with (r-1) (p-1) degree of freedom again, we are often more interested in the differences between means than in the means themselves. In this case the standard error of a difference.

$$S_{\bar{d}} = \sqrt{2MSE/r}$$

The (1-α) 100% confidence interval estimate, L (μ_j - μ_r)= (y_i–y_r) $\pm t_\alpha \sqrt{2MSE/r}$ where, again, t_α is the two-tailed t with (r-1) (p-1) df. If we want to test the significance between two means, we can use t as a test statistic under certain restrictions, which we discuss later. We compute.

$$t = \frac{\bar{y}_j - \bar{y}_j}{\sqrt{2MSE/r}}$$

If t (sample t with sign ignored) is greater than the 1% t with (r-1) (p-1) degree of freedom the difference is said to be highly significant (* *). If it is less than the 1% t but greater than the 5% t,

the difference is significant (*), and if it is smaller it is smaller than the 5% t, the difference is not significant (NS).

Estimation of Genetic Variability:-

Following different parameters were used to estimate the genetic variability present among the 81-germplasm lines for periodic growth parameter, height (cm).

Arithmetic Mean:- The arithmetic mean is defined as the sum of the values of individuals in the data divided by their number. It is computed as follows. $x = (\Sigma x)/N$

Where, x = Arithmetic mean, Σ = summation, x = an observation and N = number of observations in a sample.

Standard Deviation :- It is the square root of variance and it is denoted by s or SD (in case of sample), or as σ (in the case of population) following formula. $SD=\sqrt{s^2}$

Variance:- It is expressed as the sum of squares of the deviations of all observations of a sample from its mean and divided by degrees of freedom (N-1). It is generally denoted by s^2 or V for estimates from its samples, and by σ^2 for those from populations. It is estimated by the following formula.

$$s^2 = \frac{\sum x^2 - \frac{(\sum x)^2}{N}}{N-1}$$

Where, Σ, x, x^2 and N = Summation, an observation, square of an observation, and number of observations respectively.

Standard Error:- It is a measure of the mean difference between sample estimate of mean (x) and population parameter (μ(, i.e., it is the measure of uncontrolled variation present in a sample. It is estimated by dividing the estimate of standard deviation by square-root of the number of observations in the sample, and is denoted by SE. Thus, SE = SD / √N

Where, SD = standard deviation, and N = number of observations.

Coefficient of Variance:-

The ratio of standard deviation of a sample to its mean expressed in percentage is called coefficient of variation. Following formula was used for computation of coefficient of variation.

$$CV = \frac{\sqrt{Error Variance(MSe)} x100}{G.M.}$$

Where, SD, general mean, MSe, G.M. are standard deviation, mean, error variance and grant mean respectively.

Phenotypic, Genotypic and Environmental Coefficients of Variation:- The coefficient of phenotypic, genotypic, and environmental variation were calculated as per the formula given by Burton and de-Vane (1953).

Genotypic Variance (Vg) = $MS_t - MS_e/r$

Environmental Variance (Ve) = Vg + Ve

Phenotypic Coefficient of Variance (PCV) = $\sqrt{Vp}/X \times 100$

Genotypic Coefficient of Variance (GCV) = $\sqrt{Vg}/X \times 100$

Environmental Coefficient of Variance (ECV) = $\sqrt{Ve}/X \times 100$

Where, MS_t, MS_e, X and r are mean square for the treatments, mean error variance, mean and number of replications, respectively.

Estimates of Broad sense Heritability $(h)^2$ - The ratio of genotypic variance to the phenotypic variance or the total variance is known as heritability (broad sense). Thus heritability is the heritable portion of phenotypic variance. According to Falconer (1996) It is a good index of the transmission of characters from parents to their offspring. It is calculated from total genetic variance, which consists of additive, dominance and epistatic variance. It is calculated with the help of following formula.

h^2 (bs) = $[Vg/Vp] \times 100 = [Vg/(Vg+Ve)] \times 100$

Where h^2, V_g, V_p and V_e are heritability (bs) genotypic, phenotypic, and environmental variance respectively.

Estimates of Genetic Advance:- Improvement in the mean genotypic value of selected plants over the parental population is known as genetic advance. It is the measure of genetic gain under selection. Genetic advance was calculated by following formula.

$Gs = (K) (\sqrt{V_p}) (H) = (K) (V_g) / \sqrt{V_p}$

Gs (% of mean) = $(K) (V_g) \times 100 / (\sqrt{V_p} \times \text{mean})$

Where Gs, K, H, V_g, and V_p are genetic advance, selection differential at 5% selection intensity (2.06), heritability (V_g/V_p), genotypic variance and phenotypic variance respectively.

Simple Correlation Coefficient:- Karl Pearson and Lee (1902) has developed such a coefficient, which may measure the degree of relationship or association between two variables X and Y and is represented by the symbol r. In term of variances of X and y used following formula. $r = Cov.\ (XY)/\sqrt{\sigma x^2\ \sigma y^2}$

It is also written a – $r = MSP_t / \sqrt{MS_{tx}.\ MS_{ty}})$

Where r, Cov. (XY), σx^2, σy^2 MSP_t MS_{tx} and MS_{ty} are simple correlation coefficient, covariance (XY), variance x and variance y, mean sum of products of genotypes, mean sum of square of treatments for the variable x and mean sum of square of treatments for the variable y, respectively.

Genotypic, Phenotypic and Environmental Correlation Coefficient:- The correlation coefficient at genotypic, phenotypic and environmental levels, which were calculated from the variance and covariance according to Johnson *et al.* (1956).

Phenotypic Correlation Coefficient: - The association between two variable, which can be directly observed. It is worked out from phenotypic variances and co variance. It is computed using following formula.

$$r_p = PCOV_{xy} / \sqrt{(PV_x,\ PV_y)}$$

Where, r_p, $PCOV_{xy}$, PV_x, and PV_y are phenotypic correlation, phenotypic covariance of xy, phenotypic covariance of x and phenotypic covariance of y respectively.

Genotypic Correlation Coefficient:- The inherent or heritable association between two variables is known as genotypic correlation. This type of correlation may be either due to pleiotropic action of genes or due to linkage or more likely both. It is calculated with the help of following formula.

$r_g = GCOV_{xy} / \sqrt{(GV_x, GV_y)}$

Where, r_g, $GCOV_{xy}$, GV_x, and GV_y are genotypic correlation, genotypic covariance of xy, genotypic covariance of x and genotypic covariance of y respectively.

Environmental Correlation Coefficient:- The association between two variables, which is entirely due to environmental effect. It is estimated fro error variances and co variances. It is calculated by following formula.

$$r_e = ECOV_{xy} / \sqrt{)EV_x, EV_y)}$$

Where, r_e, $ECOV_{xy}$, EV_x and EV_y are genotypic correlation, genotypic covariance of xy, and genotypic covariance of y respectively.

Phenotypic Stability Analysis:-

Stability in performance is one of the most desirable properties of a genotype to be released as a variety for wide cultivation. A number of statistical methods are now available for estimation of phenotypic stability, for this purpose the multilocational trials over a number of years are conducted. Sometime the unilocational trials can also serve the purpose provided different environmental are created by planting experimental material at different level of

fertilizer, irrigation, sowing dates etc. The data thus, obtained are subjected to environment-wise analysis of variance followed by pooled analysis of the data.

1. Finlay and Wilkinson Model (1963). In this method GxE interaction is partitioned in to two components: regression and deviation from regressions. The sums of squares for genotypes, environments, GxE interaction, blocks within environments and residual (error) can be obtained by a routine method using mean values averaged over blocks. The sums of squares due to regression can be calculated as:

$$\text{SS regression} = \sum_{i}\left[\left(\sum_{i} Y_{i}\, i\right)' \Big/ \sum_{i} I^{2}_{j}\right] - \text{SS environments}$$

$$= b_i \sum_{j} Y_{ij} I_{j} - \text{SS environments}$$

Where = I_j is the envir onmental index

b is the regression v

The environmental index

I_j = mean of J[th] environment – overall mean

$$\text{or } I_j = \frac{\sum_i Y_{ij}}{g} - \frac{\sum_i \sum_j Y_{ij}}{ge}$$

The regression coefficient for each genotype can be calculated as:

$$b_i = \frac{\Sigma_j Y_{ij} I_j}{\Sigma_j I_j^2}$$

Where, $\Sigma_j Y_{ij} I_j$ is the sum of products of the mean (M) of that variety with its corresponding environmental index

and $\Sigma_j I_j^2$ is the sum of squares of environmental index values and thus will be a common value for each regression coefficient the values of $\Sigma_j Y_{ij} I_j$ can be obtained as

[M] [I_j] = [S]

where [M] is the matrix of genotypes means

[I] is the vector for environmental index

[S] is the scores of the sum of products

Analysis of variance for GxE interaction as per Finlay and Wilkinson, 1963.

Source of variation	**d.f.**	**SS**	**MSS**
Genotypes	g-1	-	Mg.
Environments	e-1	-	Me
GxE interaction	(g-1) (e-1)	-	Mg x e
Regressions linear	g-1	-	-
Deviation from regressions	(g-1) (e-2)	G x Ess – reg. SS	Md.
Replicates within environments	e(r-1)	-	-
Residual	e(g-1) (r-1)	-	-

In this model the mean yield (y) of all the genotypes for each environment i.e. L_1, L_2, L_3 ....L_n, allotted a quantitative grading of the environments, than the linear regression of the mean values for environments was estimated thus :

$$Y_1 - Z\,(1-\alpha)\,[(bi-1)^2 S^2 j\,(1-1/q)]^{1/2}$$

These values are similar to those of Eberhart and Russell residual mean sum of squares i.e. $Y_1 - Z(1-\alpha)[(bi-1)^2 S^2 j\,(1-1/q) + S_1{}^2]^{1/2}$

Where

$$S_j^2 = \frac{\sum_{j=1}^{q} (Yj - Y)^2}{(q-1)}$$

2. Eberhart and Russel model (1966) – Although the pooled analysis of variance provides the useful estimate, yet the information about adaptation of individual genotypes could not be available from the conventional method. Hence, the method suggested by Finlay and Wilkinson (1963), which was later on modified by Eberhart and Russel (1966) and was also applied in this investigation in order to obtain the estimate of various stability parameters for each genotypes under consideration. The stability analysis technique partitions the genotype X environment interaction components of variance of each genotype into two parts. Therefore, each genotype is characterized by three parameters viz.; (A) mean yield (x) over all environments, (B) a linear regression

coefficient (b_i) in relation to environment index and (C) the deviation from linear regression ($S^2_{d_i}$).

Since, the average slope for the environmental index is 1.0, regression coefficient for each genotype may be 1.0 or greater or lesser than one. The genotype with regression value of 1.0 is considered to have an average adaptability, where as the value less than 1.0 or higher than 1.0 would mean below average and above average adaptability respectively.

Another stability parameter ($S^2_{d_i}$=0) is considered to be stable as suggested by Singh and Chaudhary (1985).

The statistical procedures adopted for the adaptability and stability analysis (Table 1.6) of the genotypes were those proposed by Eberhart and Russel (1966). As described by Eberhart and Russel (1966), the behavior of the cultivars was assessed by the model

$$V_{ij} = m + \beta_{iIj} + \delta_{ij}\, \varepsilon_{ij},$$

Where Y_{ij} = observation of the i-th (i = 1, 2, .., g) cultivar in the j-th (j = 1, 2, ...n) environment, m = general mean, β_i = regression coefficient, I_j = environmental index obtained by the difference among the mean of each environment and the general mean (Σ_{ij} = 0), δ_{ij} = the regression deviation of the i=th cultivar in the j-th environment and C_{ij} = effect of the mean experimental error.

Source of variation	Degree of freedom	Sum of square	Expectation of mean square
Genotype	s-1	$\frac{\sum_i Y_i^2}{t} - \frac{\sum Y_{i.}^2}{ts}$	MS_1
Environ.+ Genotypes Environ.)	s(t-1)	$\sum_i \sum_j Y_{ij}^2 - \frac{\sum Y_{i.}^2}{t}$	
Environment (Linear)	1	$\frac{1}{s}\left[\frac{\left(\sum_j Y_{.j} I_j\right)^2}{\sum_j I_j^2}\right]$	
GXE (Linear)	s-1	$\sum_i \left[\frac{\left(\sum_j Y_{ij} I_j\right)^2}{\sum_j I_j^2}\right] - \frac{1}{s}\left[\frac{\left(\sum_j Y_{.j} I_j\right)^2}{\sum_j I_j^2}\right]$	MS_2
Pooled deviations	s(t-2)	$\sum_i \sum_j \delta_{ij}^2$	MS_2
Genotype-1	(t-2)	$\left\{\left(\sum_i Y_{ij}^2\right) - \frac{(Y1.)^2}{t}\right\} - \frac{\left(\sum_j Y_{ij} I_j\right)^2}{\sum_j I_j^2} = \sum_j \delta_{ij}^2$	-
Genotype-1	(t-2)	do	
Genotype-1	(t-2)	$\left\{\left(\sum_i Y_{sj}^2\right) - \frac{(Ys.)^2}{t}\right\} - \frac{\left(\sum_j Y_{sj} I_j\right)^2}{\sum_j I_j^2} = \sum_j \delta_{sj}^2$	
Pooled error	t(r-1) (s-1)		MS_4
Total			

Estimation of Stability Parameters: - The regression coefficient (b_i) and mean square deviation from the linear regression were estimated as follows :

Varieties	$\sigma^2_{v_i}$	b_i	$\sum_j Y_{ij} I_j$	$b_i \sum Y_{ij} I_j$	$\sum \delta^2_{v_i} = \sigma^2_{v_i} - b_i \sum_j Y_{ij} I_j$
1					
2					
3					
4					
5					
6					
7					
	$\sum \sigma^2_{v_i}$				$\sum_i \sum_j \delta^2_{ij}$

Where, [Σy] = Variance due to regression,

Se = the estimate of pooled error,

e = Number of environments,

g = Number of genotypes

r = Number of replications.

Computation of Regression Coefficient (b_1) The regression coefficient, which is the regression of the performance of each

genotype under different environment on the environmental means, was estimated as follow :

$$b_i = \Sigma_i Y_{ij} I_j / \Sigma_j I_j^2$$

Where,

$Y_{ij}I_j$ = sum of products of environmental index (I_j) with corresponding mean of that genotype in each environment (Y_{ij}).

$\Sigma_j I_j^2$ = sum of squares of the environmental index (I_j)

a) for each value of regression coefficient I_j is commond and equal to

$$S_i I_j^2 = I_i^2 + I_i^2 + \text{---------} + I_i^2 + \text{-----------} + I_g^2$$

b) On the other hand, $Y_{ij}I_j$ for each genotype is the sum of products of environmental index (I_i) with the corresponding mean of that genotype in each environment. These values may be obtained in the following manner.

$$[X] \times [I_i] = [\Sigma_i Y_{ij} I_j] = [S]$$

Where,

[X] = matrix of mean

$[I_j]$ = vector of environmental products i.e., $Y_{ij}I_j$

Tests of significance – The following tests of significance were carried out :

i) To test the significance of differences among genotypes mean,

$$H_0 = \mu_1 = \mu_2 = \text{-----------------} = \mu_g$$

$$F = \frac{MS_g}{MS_{P\,Deviation}} = \frac{MS_1}{MS_3}$$

ii) To test that the genotypes did not differ due to regression on environmental index i.e.,

$$H_0 = b_1 = b_2 = \text{-----------------} = b_g$$

The 'F' test used was $$F = \frac{MS_{g\,P\,Deviation}}{MS_{P\,Deviation}} = \frac{MS_2}{MS_3}$$

ii) Individual deviation from linear regression was tested as follows :

F = $[\Sigma_j S_{ij}^2/e\text{-}2]$/pooled error – t value at 5% level

P = 0.05 at (g-2) df.

iii) The hypothesis that any regression coefficient did not differ from unity or from zero was tested by the appropriate 't' test i.e. For t = 1-b/Se (b)

P = < 0.05 for (g-2) df Se (bi) = $\sqrt{[\Sigma_j S_{ij}^2/e\text{-}2\Sigma_j I^2]}$

Stable Genotype – A genotype with unit regression coefficient (b_i = 1) and the deviation not significantly differing from zero ($S_{d1}^2 = 0$) was taken to be stable genotype with unit response.

$$MS = \frac{b1-0}{Se_{b1}} \quad x_{b_1} = \frac{\sum i_{b_1}}{g} \quad s_{e_{b_1}} = \frac{\sqrt{MS_{PDeviation}}}{\sum_J I_J^2} \quad x = \frac{GrandTotal}{N} \quad Se\frac{\sqrt{MS_{PDeviation}}}{N-1}$$

3. Perkins and Jinks model (1968a) – The mean values recorded for 10 characters in respect of 25 genotypes in 24 environments as well as pooled over the environments were used for

stability analysis following Perkins and Jinks (1968a) model which is a combined statistical and genetical approach. The biometrical genetic model is given as under :

$$Y_{ij} = m + d_j + C_j + g_{ij} + e_{ij}$$

Where,

Y_{ij}	=	variety mean of i^{th} variety in the j^{th} environment.
m	=	grand mean over all the genotypes and environment
d_I	=	additive genetic effect
C_j	=	additive environmental effect g_{ij} = G x E interaction effect
C_{ij}	=	residual error variation of i^{th} variety in j^{th} environment

All these effects are assumed to be fixed. The parameters are said to be genetic in nature. Different components may be computed as under:

m	=	y......../st
di	=	$(Y._j/t) - m$
e_j	=	$(Y._j/t) - m$
Where, S	=	the total number of environments
t	=	the total number of genotypes,

It is known that G x E interaction of any variety is a linear function of environmental value, that is, $g_{ij} = b_i e_i + \delta$

So, the model becomes $Y_{ij} = m + d_i + (1 + b_i) e_j + \delta_{ij} + e_{ij}$

Where,

$$bi = (\sum_j g_{ij} e_j)^2 / \sum_j e_{j^2} \text{ and } (1 + b_i) = \sum_j Y_{ij} e_j / \sum_j e_{j^2}$$

For each variety, the regression S.S. is obtained as:

$(1 + b_i)^2 \sum_j e_{j^2} = \sum_j Y_{ij} e_{j^2} / \sum_j e_{j^2}$ and deviation from regression S.S. = $\Sigma_j \Sigma_{ij}^2$.

each mean square can be compared with the σ^2e, the error mean square, but in order to show that regression mean square accounts for a significantly larger portion of the total variation, it should be compared with : $\frac{\sum_j \delta_{ij}^2}{s-2}$ **Since** $\frac{\sum_j Y_{ij} e_j}{\sum_j e^{*2}} = (1 + b_i)2 \sum_j e_j^2$

For the regression mean square, it is apparent that we are testing the hypothesis that a significant portion of the variation of the j^{th} variety over environments is accounted for by fitting the regression slope of (1+bi). This, however, accounts both for additive environmental variation and that part of the G x E interaction variation which is a linear function of the environmental values. The significance of b_i was, therefore, tested as the difference between ($1+b_j$) and one he b_i values for the different lines were compared by .... a joint regression analysis based on the comparison ($1+b_j$) values which gives: Σ_i (reg. S.S.) = $(1+b_i)^2 \Sigma_i e_j^2$ and since $\Sigma b_i = 0$, this becomes = t $\Sigma_i e_j^2 + \Sigma_i b_j^2 \Sigma_i e_j^2$. The joint regression S.S. is t $\Sigma_i e^2 j$ and equals in this analysis to the environmental S.S. The heterogeneity between regressions S.S. is $\Sigma_i b_j^2 \Sigma_i e_j^2$. The expectations of mean squares are the joint regression analyses are sown in Table 3.8 and

r, s and t indicates number of replications, environments and genotypes, respectively.

Test of significance :

(a) The mean squares:- Mean squares due to genotypes, environments, G x E interaction, heterogeneity between regression and remainder were tested against pooled error. if remainder is significant then mean squares due to genotypes, environments, G x E interaction and heterogeneity between regression were tested against remainder mean square.

(b) Stability parameters: - The stability parameters of genotypes of the evaluated characters were based on the mathematical model of Perkins and Jinks (1968a). Test of significance for stability parameters, regression coefficient (b_i) and deviation from regression is given as follows:

(i) Testing of regression coefficient (b_i) –For testing of individual b_i value 't' test was used as : $t = \frac{b_i}{se(b_i)}$ at (t-2) degree of freedom

Where, SE (bi) = $\sqrt{\frac{\Sigma_i \delta_{ij}^2}{\Sigma i_j^2}}$

I_j Environmental index – It was obtained as the mean of all the genotypes at j^{th} environment (site mean) minus grand mean, i.e., $I_j = y._j/t - y.../st$

(ii) Testing of deviation from regression ($S^2_{d_i}$) – Significance of individual $S^2_{d_i}$, was tested by 'F' test

Where, F = $[\Sigma_j \delta^2_{ij}/(s-2)]$/ Pooled error d.f.$\delta^2_e$ at (s-2) and s (t-1) (r-1).

Table 3.8 : Analysis of variance for joint regression model of Perkins and Jinks (1968a)

Source of variation	d.f.	Sum of square	Expectation of mean square
Genotypes	(t-1)	$\Sigma_j Y^2/s - Y^2/st$	$s\Sigma_j(d)^2/(t-1)$
Joint regression	(s-1)	$\Sigma_j Y^2/s - Y^2/st$	$t\Sigma_j(d_j)^2/(s-1)$
G x E	(t-1) (s-1)	$\Sigma_j\Sigma_j(Y^2_{ij}) - \Sigma Y^2/s$ or $\Sigma_j\Sigma_j(Y^2_{ij}) - \Sigma Y^2/s - \Sigma Y^2{}_j/t + Y^2/st$	
Heterogeneity between regression	(t-1)	Sj(SjYij (Y.j/ t-Y../st)^2 SjI2j – Env. S.S.	$\Sigma_i(b_i)^2\Sigma_j(e_i)^2/(t-1)$
Remainder	(t-1) (s-1)	By subtracting heterogeneity S.S. from line x env. S.S.	$\Sigma i[\Sigma j \Sigma ij^2]/(t-1)(s-2)$
Error	s(t-1) (r-1)		σ^2

4. **Freeman and Perkins Model (1971)** – The mean values recorded for 10 characters in respect of 25 genotypes in 24 environments as well as pooled over the environments were used for stability analysis following Freeman and Perkins (1971) model which is a combined statistical and genetically approach. The biometrical genetic model is given as under :

$$Y_{ijk} = m + d_i + e_j + g_{ij} + e_{ijk}$$

Where, m = general mean

d_i = additive genetic effect of i^{th} genotypes,

e_j = additive environmental effect,

g_{ij} = Genotypes – environment interaction effect, and

e_{ijk} = the error associated with k_{th} observation.

A. Estimation of environmental index = considering two replication s, there can be three different ways to estimate I_i or Z_j and to perform the analysis:

1. The values of replication two are used for measuring Z_1 and those of replication one and two for variety mean.

2. Replication two for Z_1 and replications one for mean of varieties,

3. Replication one for Z_1 and replication two for mean.

To disting the I_j values estimated in other two models from its value in this model, another symbol Z_1 was used $Z_j = Y_j - Y$

Where, $\bar{y}.. = \frac{\sum_i \sum_j y_{ij}}{N}$, Y.j = the total overall the varieties under j^{th} environment

Estimation of b_1 values : Regression coefficient is defined as the regression of mean performance (y_{ij}) on the environmental index (Z_j).

$b_i .. = \frac{\sum_j \sum_k y_{ij} Z_j}{\sum_j \sum_k Z_j^2}$, with k = 1, it become $\frac{\sum_j y_{ij} Z_j}{\sum_j Z_j^2}$, $\sum_j Y_{ij} Z_j$ is obtained by multiplying each varietal mean at jth location with its respective environmental index and then summing over all the locations.

$b_i = \frac{\sum_j y_{ij} Z_j}{\sum_j Z_j^2}$, the different regression coefficients may be obtained in following way.

The number of replications needs to be kept in mind. As $b_i = \frac{\sum_j y_{ij} Z_j}{\sum_j Z_j}$, has been calculated from one replication, Hence

$$b_i = \sqrt{\frac{\sum_j y_{ij} z_j}{\sum_j Z_j^2}}$$

D. **Analysis of variance :** Variance due to environment is divided into combined regression and environmental residual (Table 3.9). If

the former is significant in comparison to the latter, that gives the true measure of environments. Variance due to genotype x environment interaction is also divided into two parts (i) Heterogeneity of regression and (ii) residual.

'F' test ; If environment the index (1) sum of square is significant, environment index is adequately the index of additive environmental effect. If β is not significantly different from unity, then independent environmental values adequately estimate additive environment component and the Freeman and Perkins' model reduces to Perkins and Jinks' model. Following tests of significance are performed :

A. Heterogeneity of regression is against residual sum of square (2).

B. Residual interaction (G x E) sum of square against error sum of square.

C. Environmental (residual) sum of square against error sum of square.

D. Environment (combined) sum of square against environmental (residual) sum of square (1).

Calculation of standered deviation :

A. Calculation of σ^2_{vi} which is sum of square due to ith variety.

$$\sigma_{vi}^2 = \sum_i Y_{ij}^2 - \frac{1}{n} Y_i^2$$

Where, Y_{ij}^2 is number of environment of jth environment and Y_i^2 is the sum of all the environment of ith variety.

B. Calculation of $\bar{S}_{d} - \bar{s}_{d}^2 = \frac{\sum_i \delta_{ij}^2}{s-2} - \frac{s_e^2}{r}$ from (Table 3.10)

Where, $\sum_i \delta_{ij}^2 = \sigma_{v_i}^2 - b\sum_j y_{ij} z_j$ and s_e^2 is error mean square as value $\sum y_{ij} z_j$ calculated above in (2b) are based on sums over replications, instead of means, hence divide these value by number of replications i.e. 1 is the present case.

Table 3.9 Analysis of variance of multi-environment data based on the regression approach of Freeman and Perkins model, 1971.

Source	**d.f.**	**SS**	**MS**
Genotypes	g-1)	$\frac{\sum_i y_i^2}{rs} - \frac{y_{..}^2}{rsg}$	
Environments	(s-1)	$\frac{\sum_i y_i^2}{rs} - \frac{y_{..}^2}{rsg}$	
Regression	1	$\frac{\sum_i (Y_j Z_j)^2}{rg\sum_i Z_i^2}$	

Resldual (1)	(s-2)	$\left(\frac{\sum_i Y_i^2}{rg} - \frac{Y^2..}{rsg}\right) - \frac{\sum_i (Y_j Z_i)^2}{rg\sum_i Z_i^2}$	
Genotypes x invironments	(g-1) (s-1)	$\frac{\sum_i\sum_j Y_{ij}^2}{r} - \frac{\sum_i Y_i^2..}{rs} - \frac{\sum_j Y_j^2..}{rg} + \frac{Y^2...}{rsg}$	
Heterogeneity of regression	(g-1)	$\frac{\left(\sum_j Y_{ij}Z_j\right)^2}{r\sum_j Z_j^2} - \frac{\left(\sum_j Y_j Z_j\right)^2}{rg\sum_j Z_j^2}$	
Residual (2)	(g-1) (s-2)	$\left[\left(\frac{\sum_j Y_j^2}{rg} - \frac{Y^2..}{rsg}\right) - \frac{\sum_j (Y_j Z_j)^2}{rg\sum_j Z_j^2}\right]$	
Pooled Error	gs (r-1)	$\sum_i\sum_j\sum_k Y_{ijk}^2 - \frac{\sum_i\sum_j Y_{ij}^2}{r}$	

STATISTICAL ANALYSIS :

The data obtained from the selected plants were subjected to following statistical and biometrical analysis.

1. Mean

The sum of the observation divided by the number of observations the resulting figure is called as mean. Thus for

each character, data recorded from the 5 selected plants were averaged, according to the following formulae.

$$\text{Mean } (X) \frac{\Sigma X}{N}$$

Where,

ΣX = Sum of variables

N = Total number of observations

2. Analysis of variance :

The procedure for analysis of variance of each character randomized block design described as under.

Step – I

The data were arranged according to the following table for each character and treatment/variety totals (T), replication totals (R), grand totals (GT) and general means were calculated.

Treatment	**Replications**			**Total**	**Mean**
	R-I	**R-II**	**R-III**		
1	X_1 1	X_1 2	X_1 3	T_1	M_1
2	X_2 1	X_2 2	X_2 3	T_2	M_2
3	X_3 1	X_3 2	X_3 3	T_3	M_3
'	'	'	'	'	'
'	'	'	'	'	'
'	'	'	'	'	'
'	'	'	'	'	'
26	X_{26}.1	X_{26} 2	X_{26}.3	T_{26}	M_{26}
Total	R_1	R_1	R_1	G.T.	G.M.

Step – II

Calculation of sum of square

The sum of square were obtained as follows :

1. Correction factor (C.F.) $= \dfrac{(G.T.)^2}{N}$

2. Total sum of square (T.S.S.) = $(X^2{}_{1.1}$ - - - - - $X^2{}_{26.3})$-C.F.

3. Sum of square due to replication = $\dfrac{R_1^2 + R_2^2 + R_3^2}{Number\ of\ treatment}$ - C.F.

4. Sum of square due to treatment = $\dfrac{(T_1^2 + T_2^2 + T_{26}^2)}{Number\ of\ treatment}$ - C.F.

5. Sum of square due to error =

   Total sum of square – (Replication sum of squares + Treatment sum of square)

Step – III

The sum of squares are them tabulated in the ANOVA table, to test the significance between treatments which is as given below :

Source of variance	**d.f.**	**S.S.**	**M.S.S.**	**Variance ratio**	**F value**	
					5%	**1%**
Rep.	(r-1)=2	R	V_r	V_t/V_e		
Treat.	(t-1)-25	T	V_t			
Error	(r-1) (r-1)=50	E	V_e			
Total	(rt-1)=77	T.S.S.				

If the calculated value of variance ratio of greater than the F table value at 5% and 1% level of significance for the treatment degrees of freedom (25) and error degrees of freedom (50), the varietal differences are considered to be significant.

3. Component of variances

These were calculated by the formulae suggested by Burton (1952).

(i) Phenotypic variances = σ^2 ph = $\sigma^2 g + \sigma^2 e$

Where,

$\sigma^2 e$ = Error variance

$\sigma^2 g$ = Genotypic variance

(ii) Genotypic variances (σ^2 g)

$$\sigma^2 g = \frac{V_t - V_e}{r}$$

Where,

V_t = Treatment mean sum of squares

V_e = Error mean sum of squares

R = Number of replications

4. COEFFICIENT OF VARIABILITY

These were calculated by formula suggested by Burton (1952).

(i) Phenotypic coefficient of variability (PCV)

$$PCV = \sqrt{\frac{\sigma 2\ ph}{X}} \times 100$$

(ii) Genotypic coefficient of variability (GCV)

$$GCV = \sqrt{\frac{\sigma 2\ g}{X}} \times 100$$

Where,

σ^2 pH and σ^2 g are phenotypic and genotypic variances respectively.

X = General mean of the characters

5. ANALYSIS OF CO-VARIANCE :

The method used to the analysis of covariance is stated as under : -

(i) Calculation of different sum of products :

1. Correction Factor = $\frac{G.T.\ (x) \times GT\ (y)}{N}$

2. Total sum of products (TSP) = $X_{1.1} \ldots Y_{1.1} + X_{1.2}\, Y_{1.2} + + X_{26.3}\, Y_{26.3} = X_{ij}\, Y_{ij}$

3. Replication sum of products (RSP) =

$$\frac{(R_1x\ R_1y + R_2x + R_3x\ R_3y)}{26} - C.F.$$

4. Treatment sum of products (Tr.S.P.)

$$\frac{(T_1x\ T_1y + T_2x + T_2y + \ldots\ldots.T_{26}x\ T_{26}y)}{03} - C.F.$$

5. Error S.P. = Total S.P. – (Replication S.P. + Treatment S.P.) -

On the basis of above calculation, the calculated value are arranged in ANCOVA table, which is mentioned below –

ANCOVA

Source of variance	d.f.	S.S.	M.S.S.	Variance ratio
Replication	(r-1)	P_R	MSP(R)	
Treatment	(t-1)	P_T	MSP(T)	Spt/spe
Error	(r-1) (r-1)	SP_e	MSP(E)	
Total	(rt-1)=77			

6. ANALYSIS OF CORRELATION COEFFICIENTS :

Correlation coefficient is the mutual association between variables without employing any cause and effect relationship. The correlation coefficient between depended and independent variables are calculated with the help of following formula.

1. Correction Factor = $\frac{\text{Cov. }(x, y)}{\sigma x\ \sigma y}$

Where σx and σy are standard deviation of x and y variables or

$$r(x\,y) = \frac{\text{Cov.}(x, y)}{\sqrt{\sigma^2 x \; \sigma^2 y}}$$

Where σ^2 x and σ^2y are the variance of x and y respectively.

(i) **Genotypic correlation coefficient.**

Genotypic correlation coefficient was calculated by the formula suggested by **Robinson *et al.*, (1951)** as under –

$$\text{Genotypic correlation (rg)} = \frac{\text{Genotypic covariance (xy)}}{\text{G.V. for (X) G.V. for (Y)}}$$

Where,

(i) G.V. for X = genotypic variance for X

(ii) G.V. for Y = genotypic variance for Y

X and Y are two variables

$$\text{(a) Genotypic covariance} = \frac{\text{M.S.P. treatment XY-MSP error XY}}{\text{Number of replications}}$$

$$\text{(b) Genotypic covariance (X)} = \frac{\text{M.S.S. treatment X-MSS error X}}{\text{Number of replications}}$$

$$\text{(c) Genotypic variance (Y)} = \frac{\text{M.S.S. treatment Y-MSS error Y}}{\text{Number of replications}}$$

(ii) Phenotypic correlation coefficient.

The phenotypic correlation coefficient was calculated by the formula suggested by **Robinson *et al.* (1951)**

$$\text{Phenotypic correlation coefficient (rph)} = \frac{\text{Phenotypic covariance (XY)}}{\text{Ph. V. (X). Ph. V. (Y).}}$$

Where,

Ph. V. for X = Phenotypic variance for X

Ph. V. for Y = Phenotypic variance for Y

X and Y are two variance

Phenotypic covariance=genotypic covariance + error covariance

$$= \sigma^2 g\,(Y) + \sigma^2{}_e\,(Y)$$

(iii) Test of significance of genotypic and phenotypic correlation coefficient.

To test the correlation coefficient we follow formula as suggested by **Fisher & Yates (1938)** is as under –

$$t = \frac{r\,(\sqrt{n\text{-}2})}{\sqrt{1\text{-}r^2}} \text{ at n –2 treatment d.f.}$$

Where,

r = Correlation coefficient

n = number of treatments

These are tested with the table value of correlation coefficient as suggested by Fisher and Yates (1938) at (n-2) treatment degree of freedom 5%, 1% level of significance. It the

calculated value of correlation coefficient is greater than the table value, it is considered to be significance.

7. PATH COEFFICIENT ANALYSIS :

The original concept of path coefficient was proposed by **Wright (1921)** and later elaborated by **Wright (1934)**. If the cause and effect of relationship is well defined, it is possible to represent whole system of variables in the form of diagram known as path diagram. The path coefficient analysis is the simply standardized partial regression coefficient which splits the correlation coefficients into the measures of direct and indirect effects of a set of independent variables on dependent variables.

The path analysis unravels whether the association of these characters with yield is due to their direct effect on yield or is a consequence of their indirect effect via some other traits.

Path analysis is worked out by using the estimates of correlation coefficients, all possible correlations among the dependent and independent should be worked out. Path analysis taken into three steps.

i. Calculation of direct effects
ii. Calculation of indirect effects
iii. Calculation of residual effects.

1. Calculation of direct effects.

To estimate the direct effect of different component traits simultaneous equations are developed and path coefficient for direct effect can be obtained by solving these equations.

$$r_{ny} = P_{ny} + r_{n2} P_2 y + r_{n3} P_3 y + \ldots\ldots\ldots\ldots$$

Where,

r_{iy} = represents correlations between one component character and yield.

P_{iy} = represent the path coefficient between character and yield.

Piy = represents correlation coefficient i^{th} of character to j^{th} character.

Above formulated simultaneous equation can be presented in the matrix form, which is as follows –

$$\begin{array}{ccccc} \text{Matrix A} & & \text{Matrix B} & & \text{Vector C} \\ \left|\begin{matrix} r_1y \\ r_2y \\ \vdots \\ r_{ny} \end{matrix}\right|_{n\times1} & = & \left|\begin{matrix} 1 & r_{12} & r_{13} & r_{1n} \\ r_{21} & 1 & r_{23} & r_{2n} \\ \vdots & \vdots & \vdots & \vdots \\ r_{n_1} & r_{n_2} & r_{n_3} & 1 \end{matrix}\right|_{n\times n} & \times & \left|\begin{matrix} P_1y \\ P_2y \\ \vdots \\ P_{ny} \end{matrix}\right|_{n\times1} \end{array}$$

$$\underline{A} = \underset{\sim}{B}\,\underline{C}$$

Where,

r_{ij} = r_{ji} and so on

r_{ij} = correlation of each component characters to yield.

P_{iy} = Direct effect of 1^{st} character on yield and so on.

When the B matrix is inverted (B^{-1}) then the path coefficient P_{ij} were obtained as follows :

Where, $P_{ij} = A.B.^{-1}$

i = number of row

j = number of column

ii. Calculation of indirect effects.

The indirect effect can be calculated by multiplying the values of direct path coefficients to the correlation coefficients of respective rows and column.

Indirect effect = $r_{ij} \times P_{ij}$

P_{ij} = Direct effect of i^{th} character to yield.

iii. Calculation of residual effects.

The residual effect can be calculated by the following formula.

Residual effect = $1 - R^2$

Where,

$$R^2 = P_{1Y} . r_{1y} + P_{2y}\, r_{2y} + \ldots\ldots\ldots\ldots P_{ny}\, r_{ny}$$

8. ESTIMATION OF HERTIABILITY AND GENETIC ADVANCE

Heritability

Heritability in broad sense, is the ratio of genotypic variance to the phenotypic variance. It is calculated by using the formula suggested by **Burton and Devane (1953)**.

$$h^2 = \frac{\sigma^2 g}{\sigma^2 g + \sigma^2 e} = \frac{\sigma^2 g}{\sigma^2 ph}$$

Where,

$\sigma^2 g$ = Genotypic variance

$\sigma^2 e$ = Environmental variance or error

$\sigma^2 ph$ = Phenotypic variance

Genetic advance.

Expected genetic advance is estimated by using the method suggested by **Allard., (1960)**

$$G.A. = \frac{\sigma^2 g}{\sigma^2 ph} . K \sigma ph$$

$$= h^2 . K. \sigma ph.$$

Where,

K = Selection differential at 5% selection intensity (i.e. 2.06)

Genetic advance as per cent of mean (G.A.%)-

$$G.A. (\%) = \frac{\text{Genetic advance}}{X} \times 100$$

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Experimental Findings

Chapter-IV

EXPERIMENTAL FINDINGS

CORRELATION COEFFICIENT ANALYSIS

The correlation coefficients were estimated for all the characters under study with seed yield and among the characters themselves both genotypic and phenotypic levels. The calculated values at both, genotypic and phenotypic levels have been presented in Table 7.

(A) Association of different characters with seed yield:

The results indicated that seed yield per plant was found to be highly significant and positively correlated at both genotypic and phenotypic levels: with number of primary branches, (r_g = 0.843, r_{ph} = 0.549), number of secondary branches (r_g = 0.290, rph = 0.263), 1000-seed weight (rg = 0.398, r_{ph} = 0.364), oil per cent (rg = 0.416, rph = 0.280).

Seed yield per plant showed positive but non significant association with plant height (rg = *0.155,* rph = *0.143),* length of main raceme (rg = 0.106, rph = *0.107)* both at genotypic and phenotypic levels.

Seed yield per plant showed negative but non significant correlation with days *to* 50 per cent flowering (rg = -0.193, rph

= 0.158), reproductive phase (r = -0.087, rph = -0.061) both at genotypic and phenotypic levels.

Seed yield per plant showed negative and. significant correlation with days to maturity (r = -0.360, rph = -0.263) both at genotypic and phenotypic levels.

(B) Association among yield contributing characters:

The association of plant height with length of main raceme (rg = be.634, rph = 0.621) was found to positive and significant both at genotypic and phenotypic level. The association of plant height with number of primary branches (rg = 0.251, rph = 0.196) was found positive and significant at genotypic level only.

The association of plant height with number of secondary branches (rg = 0.134, rph = 0.104) No. of siliquae on main raceme (rg = 0.157, rph = 0.115), 1000-seed weight (1'8 = 0.161, rph = 0.126) and yield per plant (rg = 0.155, rph = 0.143) were found to be positive but non significant.

The association of plant height with days to 50 per cent flowering (rg = -0.224, rph =- 0.179) and oil per cent (r_g = -0.231, rph = -0.132) were found to be negative and significant at genotypic level only.

The association of plant height with days to maturity (rg = 0.045, rph = -0.034) was found to be negative and non significant both at genotypic and phenotypic level. Length of main raceme with number' of primary branches (rg = 0.041, rph = 0.060), number of secondary branches (rg = 0.157, rph = 0.123), 1000-seed weight (rg = 0.164, rph = 0.128) and yield per plant (rg = 0.106, rph = 0.107) were found to be positive and non significant both at genotypic and phenotypic level.

Length of main raceme with No. of siliquae on main raceme (rg = 0.229, rph = 0.190) was found to be positive and significant at genotypic level only.

Length of main raceme with days to 50 per cent flowering (rg = -0.284, rph = -0.216), oil per cent (rg = -0.289, rph = -0.183) were found to be negative and significant at genotypic level only.

Length of main raceme with days to maturity (rg = -0.075, rph = -0.021) was found to be negative and non-significant.

Number of primary branches with number of secondary branches (rg = -0.025, rph = 0.050) was found to be negative and non-significant at genotypic level while positive and non-significant at phenotypic level.

Number of primary branches with days to 50 per cent flowering (rg = 0.001, rph = -0.058) was found to be positive and non-significant at genotypic level while negative and non-significant at phenotypic level.

Number of primary branches with No. of siliquae on main raceme (rg = -0.190, rph = -0.084), days to maturity (rg = -0.197, rph = -0.092) were found to be negative and non-significant both at genotypic and phenotypic levels.

Number of primary branches with 1000-seed weight (rg = 0.033, rph = 0,004), oil per cent (rg = 0.153, rph = 0.167) were found to be positive and non-significant both at genotypic and phenotypic levels.

The association of number of primary branches with seed yield (rg = 0.843, rph = 0.549) was found to be positive and significant both at genotypic and phenotypic levels.

Number of secondary branches with days to 50 per cent flowering (rg = -0. 417, rph = -0.309) was found to be negative and significant both at genotypic and phenotypic levels.

Number of secondary branches with siliquae on main raceme (rg = 0.141, rph = 0.060), 1000-seed weight (rg = 0.003, rph . 0.014) wore found to be positive and non-significant both at genotypic and phenotypic levels.

Number of secondary branches with days to maturity (rg = 0.178, rph = -0.143) was found to be negative and non-significant both at genotypic and phenotypic levels.

Number of secondary branches with oil per cent (rg = 0.502, rph = 0.313) seed yield (rg = 0.290, rph = 0.263) were found to be positive and significant both genotypic and phenotypic levels.

Days to 50 per cent flowering with No. of siliquae on main raceme (rg = 0.547, rph = -0.464) was found to be negative and significant both at genotypic and phenotypic levels.

Days to 50 per cent flowering with days to maturity (rg = 0.37.5, rph = 0.344) was found to be positive and significant both at genotypic and phenotypic levels.

Days to 50 per cent flowering with 1000-seed weight (rg = 0.041, rph = -0.003) was found to be positive and non-significant at genotypic level while negative and non-significant at phenotypic level.

Days to 50 per cent flowering with oil per cent (rg = -0.230, rph = -0.156) was found to be negative and significant 'at genotypic level while negative and non-significant at phenotypic levels.

Days to 50 per cent flowering with seed yield (rg = -0.193. rph = -0.158) was found to be negative and non-significant both at genotypic and phenotypic levels.

Number of siliquae on main raceme with days to maturity (rg = 0.544, rph = 0.644) was found to be positive and significant both at genotypic and phenotypic levels.

Number of siliquae on main raceme with 1000-seed weight (rg = -0.475. rph = 0.339) was found to be negative and significant both at genotypic and phenotypic levels.

Number of siliquae on main raceme with oil per cent (rg = 0.050, rph = -0.028) was found to be positive and non-significant at genotypic level while negative and non-significant at phenotypic levels.

Number of siliquae on main raceme with seed yield per plant (rg = -0.087, rph = -0.061) was found to be negative and non-significant both at genotypic and phenotypic levels.

Days to maturity with test weight (rg = -0.575, rph = -0.442) and seed yield per plant (rg = -0.360, rph = -0.263) were found to be negative and significant both at genotypic and phenotypic levels.

Days to maturity with oil per cent (rg = -0.212, rph = -0.168) was found to be negative and non-significant both at genotypic and phenotypic levels.

1000-seed weight with oil per cent (rg = 0.254, rph = 0.171) was found to be positive and significant at genotypic level while positive and non-significant at phenotypic level.

1000-seed weight with seed yield per plant (rg = 0.398, rph = 0.364) was found to be positive and significant both at genotypic and phenotypic level.

Oil per cent with seed yield per plant (rg = 0.416, rph = 0.280) was found to be positive and significant both at genotypic and phenotypic levels.

PATH COEFFICIENT ANALYSIS:

The genotypic correlations of different characters with seed yield were further partitioned into direct and indirect effects which have been presented in the Table 8. The results thus obtained have been given below.

1. Plant height Vs seed yield per plant:

The genotypic association of plant height with seed yield was found to be 0.155, by partitioning of the above genotypic correlation. It was observed that plant height had negative direct effect (-0.347) on seed yield. Length of main raceme (-0.211), days to 50 per cent flowering (-0.473) had negative indirect effect on seed yield. Whereas, number of primary (0.290) branches, number of secondary (0.114) branches, number of siliquae on main

raceme (0.437), days to maturity (0.094), 1000-seed weight (0.107). oil per cent (0.144) had positive indirect effect on seed yield.

2. Length of main raceme Vs seed yield:

Character, length of main raceme had negative direct effect (-0.333) on seed yield. Character. Showing negative indirect effect via plant height (-0.220) , days to 50 per cent flowering (-0.602) . Whereas, number of primary branches (0.048) , number of secondary branches (0.134), number of siliquae on main raceme (0.635), days to maturity (0.155), 1000-seed weight (0.109) oil per cent (0-181) had positive indirect effect.

3. Number to primary branches Vs seed yield:

Number of primary branches had positive direct effect (1.156) on seed yield. The positive indirect effect were shown by days to 50 per cent flowering (0.002) , days to maturity (0.409), 1000-seed weight (0.022). The negative indirect effect were shown by plant height (-0.087), length of main raceme (-0.014) , number of secondary branches (-0.021), number of siliquae on main raceme (-0.529) and oil per cent (-0.095).

4. Number of secondary branches Vs seed yield:

Number of secondary branches had positive direct effect (0.851). The positive indirect effect were noted in number of

siliquae on main raceme (0.392), days to maturity (0.369), 100o-seed weight (0.002). Whereas, the negative indirect effect were shown by plant height (-0.046), length of main raceme (-0.052) , number of primary branches (-0.029) , days to 50 per cent flowering (-0.883)and oil per cent (-0.313.).

5. Days to 50 per cent flowering Vs seed yield:

Days to 50 per cent flowering had positive direct effect (2.117) on seed yield. The positive indirect effects were shown by plant height (0.076), length of main raceme (0.095), number of primary branches (0.001). 1000-seed weight (0.028) and oil per cent (0.144).

The negative indirect effect were shown by number of secondary branches (-0.355), number of siliquae on main raceme (-1.521) and days to maturity (-0.779).

6. Number of siliquae on main raceme Vs seed yield:

Number of siliquae on main raceme had highest positive direct effect (2.779) on seed yield. The positive indirect effect were shown by number of secondary branches (0.120). The negative indirect effects were shown by plant height (-0.055), length of main raceme (-0.076) number of primary branches (-0.220), days to 50 per cent flowering (-1.159) , days to maturity (-1.128), 1000-seed weight (-0.316) and oil per cent (-0.031).

7. Days to maturity Vs seed yield:

Character days to maturity had maximum negative direct effect (-2.075) on seed yield. The negative indirect effects were shown by number of primary branches (-0.228), number of secondary branches (-0.151) and 1000-seed weight (-0.383). The positive indirect effects were shown by plant height (0.016), length of main raceme (0.025), days to 50 per cent flowering (0.794), number of siliquae on main raceme (1. 511) and oil per cent (0.133).

8. 1000-seed weight Vs seed Yield:

1000-seed weight had positive direct effect (0.666) on seed yield. The positive ,indirect effect were shown by number of primary branches (0.038), number of secondary branches (0"0003), days to 50 per cent flowering (0.088) and days to maturity (1.193). The negative indirect effect were shown by plant height (-0.056), length of main raceme (-0.055), number of siliquae on main raceme (-1. 320) and oil per cent (-0.159).

9. Oil per cent Vs seed Yield:

Oil per cent had negative direct effect (-0.625) on seed yield.. The negative indirect effect was shown by days to 50 per cent flowering (-0.488) only whereas, the positive indirect effects were noted in plant height (0.080), number of primary

branches (0.177), number of secondary branches (0.427) length of main raceme (0.096), number of siliquae on main raceme (0.139), days to maturity. (0.440) and 1000-seed weight (0.169).

Heritability and Genetic Advance:

The heritability estimates of the character give the knowledge about their heritable nature and extent of environmental influences on their expression, while genetic advance reveals the expected genetic gain during selection. The heritability in broad sense and genetic advance in per cent of mean of different characters have been worked out in present investigation. The results are presented in Table 9.

High values of heritability were observed for seed yield per plant (95.3%), plant height (90.3%), length of main raceme (88.3%) and 1000-seed weight (80.7%).

Medium values of heritability were recorded for days to 50 per cent flowering (76.9%), number of secondary branches (74.8%), days to maturity (61.2%), secondary branches (58.9%) while oil per cent (44.4%) and number of primary branches (36.3%) showed low estimates of heritability.

The high values of genetic advance in per cent of mean were recorded for seed yield per plant (76.38), 1000-seed weight (43.27), number of secondary branches (32.34) length of main raceme (30.90).

The medium values of genetic advance in per cent of mean were recorded for days to 50 per cent flowering (17.57), plant height (15.79) and number of primary branches (15.68).

The low values of genetic advance in per cent of mean recorded for secondary branches (7.80), days to maturity (5.65) and oil per cent (4.32).

Stability Analysis:

The analysis of variance for stability parameters on the basis of performance of different test genotypes in 24 varying environments for all the ten characters using four methods are presented in table numbers 2 to 6 which revealed that there were significant differences among the genotypes over environments for all the traits studied. It is also apparent that the mean performances of the genotypes were also highly variable under different environments. More over the interaction of genotypes x environment were also significant for all the traits. It directs that the performance genotypes varied from environment to environmental therefore, it is imperative to select the stable genotypes as per environmental situations. The mean squares were also significant against reminder for all the traits except oil content considering the ANOVA of Freeman and Perkins the environment, combined regression and GxE were also highly significant for all the traits tested against error for the character concern.

Further partitioning of GxE interactions in ‾ to heterogeneity between regression and remainder showed that mean squares due to these components were significant for all the traits. This indicated the prepotency of linear component in these traits and hence, prediction appeared possible. Nevertheless, these traits had both linear and non-linear components of GxE interactions. However, non-linear component was higher than linear component for all the traits except number of primary branches per plant indicating that prediction could not be made easily for these traits. However, it could done by considering individual genotypes. Similarly, highly significant values of pooled deviations suggested that the genotypes differed consi·lerably with respect to their stability for the traits under study.

The stability analysis technique partitioned the genotype x environment interaction components of variance of each genotype in to two parts; therefore, each genotype will be characterized by three parameters i.e. mean of the genotype over all environments (x), linear regression coefficient in relation to environmental index (bi) and deviation from linear regression (S^2di). Since the average slape of the environmental index is one, regression coefficient for each genotypes may be one (unity) or greater or lesser than unity. Hence, genotype with regression value of unity is considered as to have an

average adaptability, where as the values less than unity and above unity indicates adaptability to poorer or favorable environment as per Eberhart and Russel model, 1966 but in Perkins and Jinks model, 1968 bi value >0 indicates stability in favorable environment, bi value <0 indicates stability in stress environment respectively. Another stability parameter S^2di indicates the variation displayed by the genotypes for a particular trait over environments having similar indices. In present study, a genotype with unit regression coefficient ($b_i=1$) and the deviation not significant by different from zero ($S^2di=0$) are considered as stable as suggested by Singh and Chaudhary (1985).

Keeping in view the above standards the character wise description is presented as under-

Days to flower:

For days to flower, both regression coefficient (bi) and mean square deviation S^2di values were non significant for 18 genotypes. Eleven genotypes showed significant bi values indicating the presence of linear components of GxE interactions on the other hand six genotypes showed significant S^2di values having non-linear components of GxE interactions. Eleven genotypes showed bi values more than one. Indicating their suitability in favorable environment. Seven genotypes

differed significantly having mean values more than population mean (Table 3)

None of the genotypes showed absolute norms of stability; however, genotypes NDR 850, Rohini, vaibhav and vardan can be considered as stable genotypes.

Analysis through Perkins and jinks (1968) model exhibited that sixteen genotypes had mean more than population mean (44.20). All the genotypes showed bi values more than zero indicating their suitability to favorable environments.

As per Freeman and Perkins model (1971) the regression coefficient values indicated that genotypes NDR 850, Pusa Basant, Rohini, Vaibhav Urvashi, Pusa Jaikisan and Vardan showed their mean for days to flower as less than population mean. Early flowering is desirable in mustard. on the otehr hand the regression coefficient of NDR 850, Pusa Basant, Sej-2, Rohini, Vaibhav, Pusa Jaikisan and Vardan reach to unity hence these genotypes can be considered for stable for days to flower Higher the mean value for this traits for Varuna, Krishna, RH 30, RN 393, Seeta, RH 9304 Pusa Jagannath, RLM 185, Durgamani were desirable for higher fertility levels.

As per Finlay and Wilkinson (1963) the stability analysis revealed that two genotypes namely Varuna and Pusa

Jagnnath showed maximum mean values and regression coefficient near to unity possessed general adaptability. Genotypes, NDR 850, Rohini, Vaibhav and Vardan also showed their regression values near to unity but lower the mean values than population mean. In present cropping scenario early flowering is preferable hence these can also be considered as stable genotypes for early flowering.

Primary branches per plant:

In case of primary branches per plant as per Eberhart and Russell's model sixteen genotypes showed their mean significantly superior from population mean four genotypes had regression coefficient as negative showing their suitability for poor environments. Ten genotypes showed bi values more than unity indicating their adaptability in favourable environments. Twelve genotypes shosed S^2di values as negative Genotypes namely Sej2, Durgamani, Rohini, Vaibhav and Pusa Jaikisan can be considered as stable genotypes as they have their mean values more than population mean with bi values near to one and S^2di values near to zero.

According to Perkins and Jinks model 16 genotypes showed higher mean values as compared with population mean and bi value more than one indicating their suitability to poor environment. Genotypes namely RH 819, Pusa Basant, RLM

198, RH 9304 showed negative bi values showing their suitability to poor environment, However, Sej2, Durgamani, Rohini and Pusa Jaikisan can be considered as stable genotypes for all the environments.

As per Freeman and Perkins model, the regression coefficient for primary branches reached near to unity for genotypes Krishna, NDR 850, Kranti, RLM 198, Jawahar 1, RLM 185, Rohini, Urvashi Pusa Bahar, Pusa Jaikisan and Maya. The mean values of Krishna, Kranti, Jawahar 1, Rohini and Pusa Jaikisan were more than population mean; hence these genotypes may be considered for stable in all type of fertility levels. Genotypes namely, Basanti; RN 393, Pusa Basant, Seeta, Pusa Jagannath, RH 9304, and Durgamani showed regression coefficient more than unity.

The mean values of Basanti and Pusa Basant, were less than population mean which reflected that these genotypes may be suitable for poor environment, other genotypes may be suitable for favourable environments.

As per Finlay and Wilkinson on model only four genotypes i.e. Durgamani, Rohini, Vaibhav and Pusa Jaikisan expressed their mean values more than population mean and regression coefficient near to unity hence these may be considered as average stable genotypes. Other test genotypes showed poor or average adaptability.

Secondary branches per plant:

More number of secondary branches are considered as desirable in Indian mustard. The mean performance of genotypes namely Varuna, RH 819, NDR 850, RN 393, Pusa Basant, Kranti, Sej-2, RH 9304, RLM 185, Pusa Bold, Rohini, Vaibhav, Pusa Jaikisan and Vardan were higher than population mean (Table 3). Considering the regression coefficient of genotypes approaching unity namely Varuna, Krishna, NDR 850, Pusa Basant, Kranti; RH 9304, Jawahar one, Pusa bold, Urvashi and Pusa Jaikisan, The S^2di values indicating near to zero of genotypes namely Varuna, Krishna, NDR 850, Pusa Basant, RH 9304 , Pusa Bold, Pusa Bahar and Pusa Jaikisan on the basis of these three parameters genotypes namely, Varuna, NDR 850, Pusa Basant, Kranti, RH 9304, Pusa Bold and Pusa Jaikisan may be considered as stable genotypes for the trait. Genotypes namely, Sej2, Rohini, Maya and Vardan were suitable for favourable environment while remaining genotypes showed S^2di values as negative can be favoured to poor environments as per Eberhart and Russel model.

As per Perkins and Jinks model genotypes namely Varuna, NDR 850, RN 393, Kranti, RH 9304, Jawahar 1, Pusa Bold and Pusa Jaikisan showed higher mean value and bi values near to one; hence these can be considered as stable.

Genotypes namely, Krishna, Basant, RH 30, Seeta, Pusa Jagannath, Durgamani, Vaibhav, Urvashi and Pusa Bahar showed their mean values as lower than population mean and bi values more than one; these genotypes may suitable for poor environment. Remaining genotypes can be favoured for fabourable environment.

As per Freeman and Perkins model (Table 3) the regression coefficient was near to unity for the genotypes namely Krishna, RH 30, Kranti, RLM 185, Durgamani and Maya. These may be considered as stable genotypes Varuna and RH 819 showed their regression coefficient values less than one hence may be suitable for poor environment other genotypes whose regression coefficient values are more than one may be suited to rich environment.

According to Finlay and Wilkinson model eight genotypes namely, NDR 850, RN 393, Kranti, RH 9304, Jawahar 1, Pusa bold, Urvashi, and Pusa Jaikisan possessed higher mean performance and regression coefficient near to unity means expressed stable performance other genotypes showed average or poor stability.

Height of plant:

Analysis of variance for stability parameters revealed significant values for all its components (Table 2, 2a, 2b and

2c). Analysis of stability parameters through Eberhart and Russel model revealed that regression coefficient was near to unity for RH 819, Basanti, Pusa Basant, Sej 2, RLM 198, Pusa Bold, Rohini, Maya, Vaibhav and Vardan. The deviation from regression were near to zero for RH 819, RH 30, Sej 2, RLM 198, Pusa Bold, Maya and Vardan revealed its suitability to all types of environments.

As per Freeman and Perkins model, the regression coefficient of genotypes namely Basanti, RH 30, Pusa Bold Urvashi and Maya touching the level of unity hence these may be suitable for all types of environments. Other genotypes may be suited for favourable or poor fertility conditions. None of the test genotypes showed stability behaviour (Regression values near to zero) as per Perkins and Jinks model (1968).

As per Finlay and Wilkinson (1963) model, the mean and regression coefficient values of RH 819, Basanti, Pusa Basant, RH 30, Sej 2, RLM 198, Pusa Bold, Rohini, Maya, Vaibhav and Vardan revealed their adaptability to all environments.

Length of main fruiting branch:

In case of length of main fruiting branch 19 genotypes showed their mean values as more than population mean. 9 accessions showed regression coefficient values as more than unity indicating their suitability to favourable (high fertility

levels) environment. The third stability parameter S^2di showed its value near to zero for 7 genotypes. Considering all, genotypes namely, Varuna, Krishna, RLM 198, Pusa Jaganath, Vaibhav, Pusa Jaikisan and Vardan can be considered as stable genotypes. As per Perkins and Jinks (1968) model the genotypes showed its regression coefficient values near to zero were RH 30, Seeta, Kranti and Urvashi these can be considered as suitable genotypes for low type of fertility level for the trait. Genotype RLM 1985 showed negative S^2di value (-12.5).

As per Perkins and Jinks model (1968), 22 test genotypes showed their bi values more than zero which can bi suitable for favourable environment. (Table 3). Only three genotypes namely RH 30, Seeta and Urvashi showed their bi values near to zero indicating their suitability in all types of environment. None of the genotype was found suitable for poor environment.

As per freeman and Perkins model (Table 4) The regression coefficient of genotypes namely, Seeta, Pusa Jaggannath, RH 9304, Rohini, Vaibhav and Maya were near to unity which revealed their stability for all the environments for the trait. Jawahar 1 was found suitable for rich environment, while other genotypes showed their suitability to poor environment as their regression values were less than unity, According to Finlay and Wilkinson model six genotypes have higher mean value of these genotypes also reach near to unity

the genotypes were NDR 850, Basanti, RLM 198, Vaibhav, Pusa Jaikisan and Vardan. These genotypes can be considered as stable for the trait.

Number of Silique on main raceme:

The analysis of variance for the trait showed highly significance differences for the trait the stability parameters as per Eberhart and Russel (1966) showed that 18 genotypes showed their mean value more than population mean the regression coefficient (bi) and deviation (S^2di) revealed that RH 819, Basanti, NDR 850, Pusa Jagannath, Jawahar 1, Vaibhav, Pusa Bahar and Pusa Jaikisan were near to unity and zero respectively mean fulfill the stability criteria for all types of environment.

1000-seed weight:

The mean value of the trait was 4.85. 12 genotypes showed their mean values as more than population mean. None of the genotypes showed bi value as unity. However, five genotypes namely RH 819, Krishna, NDR 850, Jawahar 1 and Vardan showed their bi values near to one. The deviation of these genotypes (S^2di) were also approaching to zero, Hence these can be treated as stable overall the environments. Nine genotypes showed their b_i values as more than one indicating their suitability to rich environment. Analysis through Perkins

and Jinks model exhibited that none of the genotypes had bi values as zero. The regression coefficient of RH 9305 (0.27) can be considered as stable. Other genotypes showed bi values as more than zero and can be suited for favourable environment. Two genotypes namely RH 30 and Seeta had bi values as less than zero showing their adaptability to unfavourable or poor environment as per freeman and Perkins model the regression coefficient values indicated that genotypes NDR 850, Kranti, RLM 198, RLM 185, Maya and Pusa Bahar were in view to considered as stable genotypes for 1000-seed weight,while other genotypes showed less than one values of regression and can be suited to poor environment. As per Finlay and Wilkinson model genotypes. Genotypes namely RH 819, NDR 850, RN 393, RH 9304, Maya, Vaibhav and Pusa Bahar showed higher per se performance in comparison to population mean coupled with near to unity for regression coefficient value as per Finlay and Wilkinson model hence can be considered as stable genotypes.

As per Finlay and Wilkinson model only two genotypes namely Pusa Bahar and Vardan were found stable as they possess higher mean and regression coefficient near to unity other genotypes showed average or poor stability.

Days to maturity:

Lower the mean value from population mean is desirable for this trait. The mean values of genotypes Basanti, Pusa

Basant, RLM 198, RLM 185 and Pusa bold were found less than population mean, The regression coefficient (bi) values of these genotypes along with S^2di fulfill the stability criteria (except RLM 185) and can be suited for all type of environments. The negatie bi values of Kranti, Pusa Jagannath and Vardan indicated their stability in poor environment while other genotypes were found suitable for favourable environment. As per Perkins and Jinks model (1968) the regression coefficient (bi) of RH 9304, RLM 185 and Pusa Jaikisan were near to zero hence can be considered as stable for all environment. Other genotypes showed their suitability to rich or poor environments.

According to Freeman and Perkins model sixteen genotypes showed their regression values near to one and can be considered as stable for all type of environments. As per Finlay and Wilkinson model. Five genotypes namely NDR 850, Basanti, Pusa Basant, Seeta and Pusa Bold showed mean values higher than population mean and regression coefficient values near to one as for earlyness point of view. These genotypes were not qualified for stable due to late maturity.

Seed yield per plant:

As per Eberhart and Russel model nine genotypes i.e. Basanti, Sej 2, Jawahar, Pusa Bahar and Vardan were found

stable for all environments. Other genotypes showed suitability to rich or poor environments. As per Perkins and Jinks model only one genotype i.e. RH 819 showed minimal value of bi and considered as stable.

As per Freeman and Perkins model, eleven genotypes, namely; Krishna, Basanti, RH 30, Kranti, RLM 185, Durgamani, Maya and Vardan expressed its regression values near to one hence may be considered as stable for all environments.

According to Finlay and Wilkinson model the regression coefficient and mean values of genotypes namely Basanti, Jawahar 1, Durgamani, Pusa Bold, Urvashi, Pusa Bahar and Vardan showed high and near to unity and can be considered as stable for all the environments. Negative the values of bi for Pusa Basant, RLM 198, Jawahar 1 and Maya showed its stability for low fertility level while other genotypes may be suited for favourable environments.

Oil content:

The stability parameters as per Eberhart and Russel model the high mean value than population mean regression coefficient near to unity and S^2 di near to zero of the genotypes namely Varuna, RH 819, NDR 850, Kranti, Sej 2, Jawahar 1, Vaibhav and Vardan showed stability for all environments while

negative regression and higher the value of S^2di showed other genotypes for suitability in poor or rich environments. As per Perkins and Jinks model Krishna, RLM 198 and Urvashi were found stable for the trait. According to freeman and Perkin model regression coefficient for Krishna, NDR 850, Basanti, RN 393, Pusa Jaikisan and Vardan showed near to unity value hence considered as stable for all environments. As per Finlay and Wilkinson model eight genotypes were found stable for oil content these were Varuna, RH 819, Seeta, Jawahar 1 Pusa Bold, Vaibhav, Pusa Jaikisan, and Vardan. Other genotypes showed suitability to rich or poor environment.

Discussion

Chapter-V

DISCUSSION

In the present investigation the association and path analysis on pooled data between various traits revealed significant positive correlation of seed yield with number of primary branches, number of secondary branches, 1000-seed weight and oil percent both at genotypic and phenotypic level. It implies strong relationship of these traits with seed yield and therefore, by increasing the value of these component traits, yield may easily be pushed up. These findings are in agreement with those of **Yadav (1983), Gupta *et al.*, (1987), Kumar *et al*, (1987), Reddy (1991).** Although percentage oil content also showed positive correlation with seed yield. But due to positive indirect effects via plant height, length of main raceme, number of primary branches, number of secondary branches and no. of siliquae per plant nullified the negative direct effect of oil per cent on seed yield and the correlation became positive. The study further revealed that some of the characters viz., plant height and length of main raceme were positively correlated with seed yield.

Correlation of yield with days to 50 per cent flowering and no. of siliquae per plant however, observed negative both at genotypic and phenotypic levels. It implies that emphasis on selection of these characters will not help in increase of seed yield. Days to maturity showed negative significant correlation with yield. This is primarily due to the more negative direct effect of days to maturity on yield.

Among the characters governing yield revealed that association of plant height was positive significant with length of main raceme both at genotypic and phenotypic levels and with number of primary branches at genotypic level only. It follows' that taller plant would contribute more to length of main raceme and number of primary branches. On the other hand plant height showed negative significant association with days to 50 per cent flowering and oil per cent at genotypic level only. It implies that taller plant would result in early flowering accompanied by less oil per cent. Plant height again showed negative but non-significant association with days to maturity both at genotypic and phenotypic levels. It implies that taller plant would attain early maturity with less oil per cent Plant height showed positive non-significant association with number of secondary branches, no. of siliquae per plant and 1000-seed weight. It suggests that taller plant would give rise to more number of secondary branches, longer number of siliquae per plant and higher test weight as these traits attribute more to yield.

Length of main raceme showed positive association with yield. **(Chaturvedi *et al.*, 1988).** Association of length of main raceme was positive significant with no. of siliquae per plant at genotypic level only which suggests that length of main raceme is a kin to no. of siliquae per plant giving overall impact on seed yield. It showed positive non-significant association with number of primary

branches, number of secondary branches and 1000 seed weight both at genotypic and phenotypic levels. It follows that more length of main raceme would attain more number of primary and, secondary branches and more 1000-seed weight. On the other hand length of main raceme showed negative and significant association with days to 50 per cent flowering and oil per cent at genotypic level only. It suggests that more length of main raceme would attain: early flowering with less oil per cent. Further, it showed negative and non-significant association with days to maturity both at genotypic and phenotypic levels. It revealed that more length of main raceme would attain early maturity.

Number of primary branches showed positive significant association with 1000-seed weight and oil per cent both at genotypic and phenotypic levels. It could be understood that more number of primary branches would attain more test weight and oil per cent. Number of primary branches showed positive and non-significant association with days to 50 per cent flowering at genotypic level while negative and non significant at phenotypic levels. On the other hand number of primary branches showed negative non-significant association with number of secondary branches at genotypic level while positive and non-significant at phenotypic levels. It suggests that more number of primary branches reduces secondary branches number. Further, number of primary branches showed negative non-significant association with no. of siliquae per plant and days to

maturity both at genotypic and phenotypic levels. It could be understood that more number of primary branches would attain less no. of siliquae per plant and less number of days to maturity.

Number of secondary branches showed significant positive association with oil per cent both at phenotypic and phenotypic levels. It revealed that more number of secondary branches would attain", higher oil per cent. Further it showed non-significant positive association with no. of siliquae per plant and 1000-seed weight. It suggests that more number of secondary branches would attain more no. of siliquae per plant and 1000-seed weight. On the other hand number of secondary branches showed significant negative association with days to 50 per cent flowering both at genotypic and phenotypic levels. It could be understood that more number of secondary branches would attain early flowering. Further it showed negative non-significant association with days to maturity both at genotypic and phenotypic levels.

Association of days to 50 per cent flowering was significant positive with days to maturity both at genotypic and phenotypic levels. It could be understood that early flowering would attain early maturity. Similar results were also observed by **Yadav *et al.*, (1978).** Further days to 50 per cent flowering showed positive non-significant association with 1000-seed weight at genotypic level while negative non-significant at phenotypic levels.

No. of siliquae per plant revealed positive significant association with days to maturity both at genotypic and phenotypic levels. It suggests that, long no. of siliquae per plant results late maturity. Further no. of siliquae per plant showed positive non-significant association with oil per cent at genotypic level while negative non-significant at phenotypic levels. It suggests that long no. of siliquae per plant results higher percentage of oil. On the other hand no. of siliquae per plant showed significant negative association with 1000-seed weight both at genotypic and phenotypic levels. It suggests long no. of siliquae per plant would attain less 1000-seed weight.

Days to maturity showed negative and significant association with 1000-seed weight both at genotypic and phenotypic levels. It suggests that more days to maturity leads to reduction of seed weight. Further days to maturity showed negative non-significant association with oil per cent both at genotypic and phenotypic levels. It also suggests that more number of days to maturity leads to the reduction of seed size and oil per cent.

Association of 1000-seed weight with oil per cent was found to be positive and significant at genotypic level while non-significant and positive at phenotypic levels. It could be understood that more 1000-seed weight results higher percentage of oil.

The genotypic correlation coefficient were further partitioned into direct and indirect effects to find out the cause and effects relationship of various traits on yield.

In the present investigation path coefficient analysis revealed that genotypic correlation of plant height with seed yield was positive. Similar findings were observed by **Chaudhary *et al.*, (1987), Kumar et al., (1987), Singh *et al.*, (1987).** Though the direct effect of plant height on seed yield was negative. This was primarily due to the positive indirect effect of number of primary, secondary branches, reproductive phase, days to maturity, 1000-seed weight and oil per cent. Other traits viz., length of main raceme and days to 50 per cent flowering have negative indirect effects. By mutual cancellation of these effects, the correlation between plant height and seed yield became positive.

The genotypic correlation between length of main raceme and seed yield was positive. Similar results observed by **Chaturvedi *et al.*, (1988).** Though the direct effect of length of main raceme on seed yield was negative. This was primarily due to the positive indirect effect via number of primary -branches, number of secondary branches, reproductive phase, days to maturity, 1000-seed weight and oil per cent. Other traits viz., plant height, days to 50 per cent flowering showed negative indirect effects.

The genotypic correlation of number of primary branches with seed yield was positive. Similar results also observed by **Chaturvedi *et al.*, (1988).** It also revealed positive direct effect accompanied by positive indirect effect via days to 50 per cent flowering days to maturity and 1000-seed weight.

The genotypic correlation between number of secondary branches and seed yield was positive. Similar results were also observed by **Chaudhary *et al.*, (1990).** This was primarily due to the positive direct effect along with positive indirect effect *via* reproductive phase, days to maturity and 1000-seed weight.

The genotypic correlation between days to 50 per cent flowering and seed yield was negative though the direct effect was positive along with positive indirect effect via plant height, length of main raceme number of primary branches, 1000-seed weight and oil per cent. Other traits viz., number of secondary branches, no. of siliquae per plant and days to maturity, showed negative indirect effect. By mutual cancellation of these effects the correlation between days to 50 per cent flowering and seed yield became negative.

The genotypic correlation between no. of siliquae per plant and seed yield was negative inspire of it having maximum positive direct effect besides similar positive indirect effect via number of secondary branches. Other traits viz., plant height, length of main raceme,

number of primary branches, days to 50 per cent flowering, days to maturity, 1000-seed weight and oil per cent showed negative indirect effect and slice off high positive direct effect to the extent that it revealed negative correlation with seed yield.

The genotypic correlation between days to maturity and seed yield was negative. This has primarily due to its high negative direct effect itself beside a negative indirect effect via number of primary branches, number of secondary branches and 1000-seed weight. Other traits viz., plant height, length of main raceme, days to 50 per cent flowering, no. of siliquae per plant and oil per cent however, have shown positive indirect effect. By mutual collection of these effect, the correlation between days to maturity and seed yield became negative.

The genotypic correlation between 1000-seed weight and seed yield was positive. **Chaudhary *et al.*, (1981)**. This was attributable to its positive direct effecc together with positive indirect effect via number of primary branches, number of secondary branches, days to 50 per cent flowering and days to maturity. Even so other traits viz., plant height, length of main raceme, no. of siliquae per plant and oil per cent have shown negative indirect effect. By mutual cancellation of these effects, the correlation between 1000-seed weight and seed yield became positive.

The correlation between oil per cent and yield was observed positive, in the face of it revealing negative direct effect coupled with negative indirect effect of days to 50 per cent flowering. Other traits viz., plant height, length of main raceme, number of primary branches, number of secondary branches, reproductive phase, days to maturity and 1000-seed weight have together showed more positive indirect effect and the correlation between oil per cent and seed yield became positive.

Heritability is an index of transmissibility of a character from parents to offspring. If the heritability estimate of any character is high it is expected that improvement of that character is possible through selection, whereas low heritability indicates that character is highly influenced by the environmental fluctuations and one has to raise a larger population for selecting desirable genotypes. In the present investigation, plant height, length of main raceme, 1000-seed weight and seed yield showed high heritability indicating that improvement can be brought about by adopting direct selection for these traits. These results are in agreements with earliar reports of **Thurling (1974), Katiyar et al. (1976). and Yadav et al. (1985).**

The moderate heritability estimates were observed for number of secondary branches, days to 50 per cent flowering, no. of siliquae per plant and days to maturity indicating that these characters can be improved by making rigorous selections only in the segregating

population. Similar findings have also reported by Tiwari and Singh (1973), Paul (1978) and Yadav (1983).

The low heritability estimates however were recorded for number of primary branches and oil per cent suggesting that the improvement through selection would not be worthwhile and render itself against selection. L *et al.* (1990) also reported low heritability for these traits.

Heritability alone does not provide an ample evidence regarding the amount of genetic progress which could be possible through selection. The heritability estimates accompanied by high genetic advance is therefore, a more reliable guide for making selections. In the present investigation, high heritability together with high genetic advance in per cent of mean were observed for seed yield per plant, 1000-seed weight, length of main raceme and number of secondary branches. It is, therefore fallows that combined force more emphasis should be laid on selections for those characters having high heritability coupled with high genetic advance.

Information about phenotypic stability is useful for the selection of crop varieties as well as for any effective breeding programmes. The phenotypic performance of a genotype is not necessarily the same under diverse-ecological conditions (Ali *et al.* 2003). Some genotypes perform well in certain environments, but, fail in several others. Genotype-environment (GxE) interactions are

extremely important in the development and evaluation of plant varieties because they reduce the genotypic stability values under diverse environments (Hebert *et al.* 1995). The concept of stability has been defined in several biometrical methods including univariate and multivariate ones have been developed to assess stability (Lin *et al.* 1986; Becker and Leon, 1988; Crossa, 1990). The most widely used one is the regresion analysis method, based on regressing the mean value of each genotype on the environmental index or marginal means of environments (Romagosa and fox, 1993; Tesemma *et al.*, 1998). A good method to measure stability was previously proposed by Finlay and Wilkinson (1963) and was later modified/improved by Eberhert and Russell (1966), Perkins and Jinks (1968), Freeman and Perkins (1971) etc. The stability of varieties was defined by high mean performance for character concerned and regression coefficient (b_i=1.0). The stability was defined as adaptation of varieties to unpredictable and transient environmental conditions and the technique has been used to select stable genotypes unaffected by environmental changes. (Allard and Bradshaw, 1964).

A number of stability studies have been carried out an different crop plants as well as on mustard in India and abroad using the method of Eberhert and Russell (1966) or Finlay and Wilkinson (1963). The comparative evaluation of more these two methods is extremely limited. Hence the main objective of this study

were to evaluate the yield and its components in Indian rape genotypes in different level of fertilizers and date of sowing with locations and to determine their stabilities using different stability parameters.

The considerable amount of genotypes environment linear component emphasized genotypes deviating four regression line of unit line could be identified. The stability of productivity for the epithets of economic importance such as yield and quality, is of interest to the plant breeder. Desirable genotypes must have low genotypic - environmental interaction for agriculturally important epithets but, on the other hand may be more flexible for the other epithets. Such genotypes are said to be 'well buffered', as these could adjust their genotypic status in response to the changing environmental conditions (Lerner, 1954). Adoption is the property of genotype or population of genotypes permitting subsequent alteration of the norms of the adaptation is response to changed selection pressure (Simmonds, 1962).

Stability in a population can be achieved by two ways:-

(1) **Individual buffering:** It is the ability of an individual genotype or a population to produce a certain narrow range of phenotypes under different environment. It comes from the genetically homogeneous population such as inbreed lines, pure lines , cultivar of a self pollinated crops.

(2) **Population buffering:** A population can be an aggregate of a number of genotypes each adapted to a some what different range of environments. It arises from the interaction of different coexisting genotypes, Allard (1961) and Finlay (1963) while working on Lima-beans and barley, respectively, reported that the advance generation hybrid population were highly buffered.

The greater magnitude of variation in regression coefficient further indicated that the genotype and different degree of individual responses well under varying level of environments. It is generally accepted that for some extent variability among environment could determine the usefulness of regression response parameters.

significant differences among the genotypes over environments for all the traits studied. It is also apparent that the mean performances of the genotypes were also highly variable under different environments. More over the interaction of genotypes x environment were also significant for all the traits. It directs that the performance genotypes varied from environment to environmental therefore, it is imperative to select the stable genotypes as per environmental situations. The mean squares were also significant against reminder for all the traits except oil content considering the ANOVA of Freeman and Perkins the environment, combined regression and GxE

were also highly significant for all the traits tested against error for the character concern.

Further partitioning of GxE interactions in to heterogeneity between regression and remainder showed that mean squares due to these components were significant for all the traits. This indicated the prepotency of linear component in these traits and hence, prediction appeared possible. Nevertheless, these traits had both linear and non-linear components of GxE interactions. However, non-linear component was higher than linear component for all the traits except number of primary branches per plant indicating that prediction could not be made easily for these traits. However, it could done by considering individual genotypes. Similarly, highly significant values of pooled deviations suggested that the genotypes differed considerably with respect to their stability for the traits under study.

Similar results have also been reported by Badwal and Labana (1989), Sharma and Roy (1993), Mahto (1996), Mahto (1999), Haider (2000), Dhillon *et al.* (2001), Gunasekera *et al.* (2003), Mahto and Mahto (2003) and Singh and Kumar (2007).

Considering the stability parameters as described by Finlay and Wilkinson (1963) Eberhert and Russell (1966), Perkins and Jinks (1968) and Freeman and Perkins (1971). The

genotypes were similar in their stability for seed yield in Finlay and Wilkinson and Eberhart and Russell models due to their regression coefficients and higher mean performance, but different in other models because in two other models as ascribed just reverse criterion in respect to regression coefficients. The genotypes found common in majority of characters were Basanti, Sej 2, Jawahar 1, Durgamani, Pusa Bold, Urvashi, Pusa Bahar, Pusa Jaikism and Vardan. A critical analysis of these genotypes showed that these genotypes were constituted through combination of different genotypes of diverse origin using multiple parents which produce non-sensitiveness in diverse environments. They may also produced greater buffering capacity over a wide range of environment.

The genotypes showing positive response in favourable environments might be due to their sensitivity to higher level of fertilizers and other favourable agronomical operation or lower buffering ability in changing environments.

The stability analysis technique partitioned the genotype x environment interaction components of variance of each genotype in to two parts, therefore, each genotype will be characterized by three parameters i.e. mean of the genotype over all environments (x), linear regression coefficient in relation to environmental index (bi) and deviation from linear

regression (S^2di). Since the average slope of the environmental index is one, regression coefficient for each genotypes may be one (unity) or greater or lesser than unity. Hence, genotype with regression value of unity is considered as to have an average adoptability, where as the values less than unity and above unity indicates adaptability to poorer or favourable environment as per Eberhart and Russel model, 1966 but in Perkins and Jinks model, 1968 bi value >0 indicates stability in favourable environment, bi value <0 indicates stability in stress environment respectively. Another stability parameter S^2di indicates the variation displayed by the genotypes for a particular trait over environments having similar indices. In present study, a genotype with unit regression coefficient ($b_i=1$) and the deviation not significant by different from zero ($S^2di=0$) are considered as stable as suggested by Singh and Chaudhary (1985).

As per Eberhart and Russel model nine genotypes i.e. Basanti, Sej 2, Jawahar, Pusa Bahar and Vardan were found stable for all environments. Other genotypes showed suitability to rich or poor environments. As per Perkins and Jinks model only one genotype i.e. RH 819 showed minimal value of bi and considered as stable.

As per Freeman and Perkins model, eleven genotypes, namely; Krishna, Basanti, RH 30, Kranti, RLM 185, Durgamani, Maya and Vardan expressed its regression values near to one hence may be considered as stable for all environments.

According to Finlay and Wilkinson model the regression coefficient and mean values of genotypes namely Basanti, Jawahar 1, Durgamani, Pusa Bold, Urvashi, Pusa Bahar and Vardan showed high and near to unity and can be considered as stable for all the environments. Negative the values of bi for Pusa Basant, RLM 198, Jawahar 1 and Maya showed its stability for low fertility level while other genotypes may be suited for favourable environments.

Summary & Conclusion

Chapter-VI

SUMMARY AND CONCLUSION

To observe the genetic variability and stability parameters; an experiment consisting 25 diverse genotypes of Indian mustard namely Varuna, RH819, Krishna, NDR850, Basanti, RN393, Pusa Basant, RH 30, Kranti, Sej-2, Seeta, RLM198, Pusa Jagannath, RH9304, Jawahar-1, RLM 185, Duragmani, Pusa Bold, Rohini, Maya, Vaibhav, Urvashi, Pusa Bahar, Pusa Jaikishan and Vardan was conducted at two location i.e. Research Farms of Brahmanand Mahavidyalaya, Rath, Hamirpur (U.P.) and Nehru Mahavidyalaya Lalitpur (U.P.) during Rabi 2005-06 (first year) at three levels of fertility. First level normal dose of fertilizers (100kgN, 60kg P_2O_5, 40kg K_2O) per hectare. Second level low dose of fertilizers (50kgN, 30kgP_2O_5, 20kgK_2O) per hectare. Third level of nil fertilizers and two dates of sowing (early and late). Early sowing last week of September and late sowing last week of October. The same experiment was also repeated during Rabi 2006-07 (Second year) on same places. The data were generated on the growth, yield and quality characters at both the places and in both the years. The data generated were subjected to different statistical and biometrical analysis as per standard procedures while stability analysis was conducted using four models i.e Finlay and Wilkinson (1963), Eberhart and Russel (1966), Perkins and Jinks (1968) and Freeman and Perkins (1971). The results described and discussed in this manuscript are summarized here as under:-

1. VARIABILTIY

All the characters showed considerable amount of variability for all the traits at all the conditions. Seed yield per plant had highest coefficient of genotypic and phenotypic variability. Phenotypic coefficients of variability were higher than their respective genotypic coefficient of variability for all the characters under study which indicated that environment play significant role in expression of characters.

2. HERITABILITY AND GENETIC ADVANCE

All the characters studied showed high heritability estimates in broad sense. Heritability estimates was observed highest for seed yield per plant followed by plant height .

Estimate of genetic advance in per cent of mean was observed highest for seed yield per plant followed by 1000-seed weight high heritability coupled with high genetic advance indicates the presence of additive gene action. The estimates of genetic advance in per cent of mean were comparatively low for oil percentage and days to maturity indicating the presence of non additive gene action.

3. CORRELATION COEFFICIENT

Number of primary branches showed the highest positive and significant correlation with seed yield. Number of secondary

branches, 1000-seed weight and oil content also showed positive and significant correlation with seed yield. The negative correlation was observed for days to maturity and secondary branches with seed yield per plant.

4 .PATH ANALYSIS

Path analysis revealed that number of siliquae on main raceme, days to flowering, number of primary branches and 1000-seed weight had high direct effects on seed yield per plant. Days to maturity and oil content showed high negative direct effect. Number of siliquae and days to maturity showed high positive indirect effects *via* 1000 seed weight.

5 STABILITY ANALYSIS

1. The stability analysis revealed significant differences for genotypes, location, years, fertility levels and their various interactions. The orthogonal partitioning of components were also significant using all the models.

2. Non-linear components of GxE were higher than linear components for all the traits except number of primary branches per plant.

3. Genotypes namely, NDR 850, Pusa Basant, Rohini, Vaibhav, Urvashi, Pusa Jaikisan and Vardan were found as stable for early flowering.

4. Genotypes Varuna, Krishna, RH 30, RN 393, Seeta, RH 9304, Pusa jagannath, RLM 185 and Durgamani were observed suitable for higher fertility level and delayed flowering.

5. Genotype Sej 2, Durgamani, Rohini, Maya and Pusa Jaikishan were found stable for primary branches per plant.

6. In case of secondary branches per plant genotype Varuna, Krishna, NDR 850, Pusa Basant, RH 9034, Pusa Bold, Pusa Bahar and Pusa Jaikishan were found stable.

7. RH 819, NDR 850, Basanti, Sej-2, RLM 198, Jawahar-1, RLM 185, Vaibhav, Pusa Bahar and Pusa Jaikishan were found stable for seliquae on main fruiting branch.

8. RH 819, Krishna, NDR 850, Kranti, Jawahar-1, Durgamani, Rohini and Pusa Bahar were found stable.

9. In case of yield per plant genotypes Basanti, Sej 2, Jawahar 1, Durgamani, Pusa Bold, Urvashi , Pusa Bahar, Pusa Jaikishan and Vardan were found stable.

10. Genotypes namely, Varuna, RH 819, Kranti, Sej 2, Jawahar 1, Pusa Bold, Vaibhav, Pusa Jaikishan and Vardan showed stability for oil content.

CONCLUSION

Considering all the characters and all the models of stability under study none of the test genotypes were found stable for all the traits. However, genotypes namely NDR 850, Sej 2, Jawahar 1, Vaibhav, Pusa Bold and Vardan were found stable for majority of the characters.

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Tables

Table-1 : General description of genotypes used in study.

Genotype/variety	Pedigree	Origin	Characteristics/Suitability
1. Varuna	Pureline selection from Varanasi Local.	Kanpur	Entire mustard growing region of the country.
2. RH 819	Derived from the cross Prakash x Bulk pollen	Hisar	Rainfed areas of North West Zone.
3. Krishna	Selection from Varuna	Pantnagar	Irrigated areas of Bihar, Delhi, Haryana, Madhya Pradesh, Orissa, Punjab, Rajasthan and Utter Pradesh.
4. NDR 850	-	Faizabad	High yielding, early, responsive to fertiliger, suitable for UP and Bihar.
5. Basanti	-	Kanupr	Early maturing, higher yielder, high oil.
6. RN 393	-	Hisar	Highly responsible to fertiliger, high yielder.
7. Pusa Basanti	-	New Delhi	Suitable for limited irrigated condition.
8. RH 30	Selection from P26/3-1	Hisar	Rainfed irrigated areas of Haryana, Jammu, Punjab, North Rajasthan, and Western Uttar Pradesh.
9. Kranti	Selection from Varuna	Pantnagar	Irrigated areas of Bihar, Delhi, Gujarat, Haryana. Orissa. Punjab, Rajasthan, Uttar Pradesh and West Bengal.
10. Sej 2	Derived from the cross early maturing Brassica juncea x synthetic amphidiploid (B. campestis Var to Ria x B nigpa)		Irrigated areas of Delhi, Haryana, Punjab and Rajasthan and rainfed areas of Assam, Bihar, Jharkhan, Orissa, Chhattisgarh.
11. Seeta	Pureline selection from germplsam collected from blest Bengal.	Kanpur	Rainfed and irrigated areas of West Bengal.
12. RLM 198	-	Ludhiana	High yielding, suitable for limited irrigated condition.
13. Pusa Jagnnath	-	New Delhi	High yielding, early maturing.
14. RH 9304	-	Hisar	Suitable for irrigated condition.
15. Jawahar 1	-	Jabalpur	High yielder, having high oil.
16. RLM 185	-	Ludhiana	Suitable for limited irrigated condition.
17. Durga mani	-		Suitable for limited irrigated condition.
18. Pusa Bold	-	New Delhi	Suitable for limited irrigated condition.
19. Rohini	Selection from Varuna	Kanpur	Suitable for Madhya Pradesh and Uttar Pradesh.
20. Maya	-	Kanpur	Suitable for late sown condition.
21. Vaibhav	Derived through biparental mating involving. Varuna, Keshri CSU 1 0	Kanpur	Rainfed and irrigated areas of Madhya Pradesh and Uttar Pradesh.
22. Urvashi	IB 1786 and 1886	Kanpur	Rainfed and irrigated areas of Madhya Pradesh and Uttar Pradesh.
23. Pusa Bahar	-	New Delhi	Rainfed and irrigated areas of Madhya Pradesh and Uttar Pradesh.
24. Pusa Jaikisan	-	New Delhi	Rainfed and irrigated areas of Madhya Pradesh and Uttar Pradesh.
25. Vardan	Derived through biparental mating & involving. Varuna Keshri CSU 10, IB 1775, IB 1786 and 1886	Kanpur	Suitable for Irrigated areas of Madhya Pradesh and Uttar Pradesh.

Table-2a ANOVA for stability parameters for yield and its components in Indian mustard as per Eberhart and Russell's, 1966.

Source of variation	d.f.	Days to flower	No.of primary branches/plant	No.of sec branches/plant	Height of plant (cm)	Length of main fruiting branch (cm)	No.of seliquae on main fruiting branch	1000-seed wt. (g)	Days to maturity	Yield/plant (g)	Oil content %
Genotypes	24	27.28**	8.25**	6.25**	70.85*	206.10*9*	1[illegible]4.60**	0.65**	66.71**	8.93**	5.15**
Env. + (GxE)	275	41.85**	6.54**	3.86**	279.74**	47.77**	51.36**	0.42**	13.53**	7.52**	2.26**
Env. (Linear)	1	2060.52**	7.47**	59.82**	11742.40**	10043.3**	11632.66**	3.39**	168.24**	503.55**	35.47**
GxE (Linear)	24	17.35**	9.80**	3.77**	279.94**	51.73**	44.83**	0.37**	32.36**	6.42**	0.54**
Pooled deviation	550	40.53**	4.27**	2.64**	39.96**	40.30**	51.38**	0.19**	6.73**	3.57**	0.92**
Pooled Error	1200	0.52	1.27	0.36	31.54	13.83	6.60	0.047	0.64	1.10	0.49
Environment	23	673.68**	4.95**	24.34**	4542.24**	5022.23**	5716.33**	0.64**	59.20**	262.76**	11.95**

** significant at p = 0.01

Table-2b Analysis of variance for stability parameters for yield and its components in Indian mustard as per Perkins and Jinks, 1968.

Source of variation	d.f.	Days to flower	No.of primary branches/plant	No.of sec branches/plant	Height of plant (cm)	Length of main fruiting branch (cm)	No.of seliquae on main fruiting branch	1000-seed wt. (g)	Days to maturity	Yield/plant (g)	Oil content %
Genotypes	24	27.28**	8.25**!	6.25***	70.82**!	206.10**!	194.60**!	0.65**!	66.71**!	8.93**!	5.15**!
Env./Joint Regression	23	41.76**	6.49**!	3.84**	728.94**!	47.67**	51.55**	0.43**!	13.54**!	7.55**	2.30**!
GxE	552	18.77**	11.40**!	4.63**!	268.44**!	45.94**!	53.22**!	0.69**!	16.52**!	9.87**!	3.41**!
Heterogeneity bet. Regr.	24	17.35**	9.86**!	3.67	279.85**!	51.47**	44.75**	0.39**!	32.76**!	4.45**	0.55
Remainder	528	40.47**	4.16**	2.72**	39.84**	40.33**	51.43**	0.20**	6.75**	3.59**	0.91*
Pooled Error	1200	0.52	1.27	0.36	31.54	13.83	6.60	0.04	0.64	1.10	0.49

** significant at p=0.01 against pooled error. ! significant against remainder

Table-2c Analysis of variance for stability parameters for yield and its components in Indian mustard as per Freeman & Perkins, 1971

Genotypes	24	2140.05	33.76	113.42	20.47	289.24	284.29	769.96	301.92	115.35	70.84
Environment	23	23209.86**	4591.80**	14327.20**	2751.91**	37847.51**	34582.66**	95706.27**	35741.17**	14586.59**	9479.20**
Combined regression	1	31087.64**	27943.36**	91120.65**	16996.58**	22548.34**	225089.20**	594724.00**	212349.19**	87110.43**	56339.29**
Residual (1)	10	32442.52	49.96	142.40	11.54	291.64	295.67	794.46	354.27	78.24	88.99
G x Env.	264	12297.66**	192.68**	554.10**	124.06**	1468.79**	1462.97**	3477.10	1366.48**	538.10**	352.57**
Heterogeneity of regression	24	43.38	19.18	77.60	1.54	108.45	109.54	587.63	278.43	56.27	51.10
Residual (2)	240	14653.69	235.47	648.57	144.65	1781.23	1692.34	4051.72	1586.21	630.09	413.84
Error bet. Replicates	600	7085.22	87.69	281.68	54.00	697.84	702.10	1783.45	547.97	236.89	151.94

** significant at $p = 0.01$

Table-3: Estimates of stability parameters for seed yield and its components in Indian mustard as per Eberhart and Russell and Perkins and Jinks (1968) model.

S. No.	Variety	Days to flower			Primary branches/plant			Sec. branches/plant			Length of main fruiting branch			Seliquae on main fruity branch		
		×	bi	S^2di	×	bi	S^2di	×	bi	S^2di	×	bi	S^2di	×	bi	S^2di
1.	Varuna	45.20	0.96	0.94	7.20	2.19	-0.03	13.30	1.12	0.02	0.20	0.91	0.06	48.52	0.87	45.46
2.	RH 819	44.53	1.62	0.49	7.00	-0.16	-0.04	11.20	0.69	-0.09	67.60	1.03	49.40	46.43	1.09	0.15
3.	Krishna	44.84	0.89	2.41	7.47	2.45	-0.02	9.60	1.19	0.04	69.90	1.21	0.16	48.10	0.89	2.27
4.	NDR 850	43.70	0.99	0.10	6.00	4.08	-0.07	11.90	1.07	0.03	71.10	1.10	120.89	49.80	0.94	0.01
5.	Basanti	44.30	0.87	0.43	5.40	1.89	0.05	8.33	1.32	-0.09	76.80	0.94	-16.32	46.20	0.82	0.09
6.	RN 393	46.73	1.26	0.75	6.57	2.09	-0.09	12.10	0.94	-0.25	79.40	0.87	6.78	46.50	1.17	0.81
7.	Pusa Basanti	44.15	1.17	1.92	5.27	-0.35	-0.07	11.00	4.05	0.02	68.62	1.23	4.33	44.06	1.06	1.76
8.	RH 30	46.36	0.77	2.69	7.17	0.67	-0.02	9.20	1.53	-0.21	74.35	0.05	30.36	48.64	0.72	2.69
9.	Kranti	44.50	1.53	3.89	7.63	0.56	-0.01	11.30	1.07	0.12	81.62	1.20	-16.59	43.20	1.38	3.85
10.	Sej 2	46.16	1.21	0.72	8.33	0.89	0.11	12.80	0.79	0.43	81.95	1.22	61.80	46.60	1.26	0.69
11.	Seeta	47.08	1.24	0.94	6.33	1.63	-0.13	10.00	1.24	-0.11	56.60	0.06	3.47	48.45	1.37	0.93
12.	RLM 198	44.20	1.16	1.94	5.37	-0.75	0.02	10.50	0.10	-0.17	69.90	1.10	0.16	45.60	1.16	1.87
13.	Pusa Jagnnath	46.18	1.07	0.09	6.20	0.67	-0.03	9.60	0.59	4.86	68.80	0.394	0.09	43.44	1.13	0.04
14.	RH 9304	45.90	0.54	0.45	7.42	-2.21	-0.02	12.80	0.98	0.03	69.40	0.37	118.23	47.00	1.11	0.46
15.	Jawahar 1	45.20	0.66	0.06	6.80	1.74	0.10	10.33	1.02	0.31	67.77	2.19	16.24	43.67	0.69	0.03
16.	RLM 185	46.17	1.26	-0.08	7.33	3.39	-0.12	11.95	1.35	-0.01	60.10	1.97	-12.45	46.10	0.72	-0.10
17.	Durga mani	45.40	0.87	-0.04	7.67	0.97	0.07	9.72	0.72	-0.30	74.00	0.47	17.21	43.54	1.21	-0.13
18.	Pusa Bold	44.80	0.80	7.91	5.57	0.56	0.45	12.85	1.06	0.07	79.66	0.36	15.92	42.80	0.86	7.80
19.	Rohini	41.90	0.96	0.02	6.90	0.97	0.02	11.60	1.57	0.98	68.80	0.91	11.86	47.63	0.92	2.65
20.	Maya	44.20	1.20	0.74	4.55	3.047	0.19	10.756	1.21	0.64	79.40	1.80	17.54	46.80	0.98	1.74
21.	Vaibhav	43.80	0.99	0.03	6.70	1.03	0.08	10.22	0.65	1.21	76.82	1.06	0.11	48.49	0.97	0.02
22.	Urvashi	42.60	0.74	2.54	5.90	1.40	1.07	7.98	1.02	0.32	83.66	0.06	11.30	47.25	1.46	0.37
23.	Pusa Bahar	44.10	1.24	0.85	5.20	0.68	1.18	8.60	2.13	0.05	61.90	1.35	7.43	46.33	1.10	.20
24.	Pusa Jaikisan	40.20	0.74	2.47	7.00	1.02	1.03	12.26	1.01	0.06	83.40	0.94	0.26	48.30	0.79	0.12
25.	Vardan	43.00	0.98	1.06	6.97	0.27	0.13	13.00	0.36	0.54	69.20	0.98	0.07	44.50	0.23	1.36
Population mean		44.20			6.20			10.20			68.20			45.27		
SEm ±		1.25	0.25		0.31	0.16		0.61	0.45		0.89			1.27	0.21	

Contd..3..

Table-3 Contd...

S.No.	Variety	1000-seed weight (g)			Days to maturity			Yield/plant (g)			Oil content %			Height of plant (cm)		
		×	bi	S^2di	×	bi	S^2di	×	bi	S^2di	×	bi	S^2di	×	bi	S^2di
1.	Varuna	6.90	1.73	-0.07	130.4	3.81	4.90	27.60	2.23	-0.02	41.20	0.98	0.04	141.2	0.89	1.21
2.	RH 819	4.90	0.89	0.09	134.9	1.21	5.81	29.76	0.10	-0.01	42.10	1.01	0.03	144.6	1.05	0.04
3.	Krishna	5.20	0.86	0.06	130.6	1.92	1.65	30.01	2.46	-0.02	40.20	0.15	0.06	154.7	1.20	0.90
4.	NDR 850	4.85	0.88	0.03	127.5	1.16	4.00	27.18	3.90	-0.08	39.00	0.95	0.04	146.8	0.62	1.46
5.	Basanti	4.25	0.45	0.04	128.0	0.96	0.03	30.25	1.03	0.04	39.60	-0.36	0.32	154.2	0.93	-1.69
6.	RN 393	4.73	0.49	-0.03	134.6	0.50	13.08	30.54	2.10	-0.01	40.40	0.37**	-0.25	152.3	0.63	3.76
7.	Pusa Basanti	4.65	0.56	0.04	131.7	1.07	0.02	28.42	-0.35	-0.07	40.00	-0.54	0.69	161.4	1.06	4.10
8.	RH 30	4.95	-0.09	0.19	137.2	2.42	1.15	26.32	0.63	-0.01	38.60	0.90	-0.05	152.7	1.01	0.07
9.	Kranti	6.10	1.25	0.00	122.6	-1.10	1.38	22.05	0.59	-0.02	38.45	1.01	0.04	160.3	1.52	3.42
10.	Sej 2	5.90	0.45	-0.02	126.8	0.85	21.82	20.35	0.92	0.09	40.20	0.98	0.03	172.2	1.10	0.06
11.	Seeta	4.72	-0.21	0.15	125.4	1.10	10.81	27.72	1.60	-0.12	42.90	1.12	-0.20	159.6	0.82	9.98
12.	RLM 198	4.98	1.24	0.07	122.7	1.55	19.13	23.38	-*0.70	0.03	40.42	0.48	0.16	130.4	0.98	0.09
13.	Pusa Jagnnath	4.83	0.26	-0.04	130.2	-1.64	1.80	28.75	0.63	-0.02	42.50	1.34	-0.18	136.9	0.82	3.21
14.	RH 9304	5.20	0.27	0.20	132.6	0.41	9.10	25.33	-2.15	-0.04	43.47	-0.59	0.68	144.3	0.87	-1.66
15.	Jawahar 1	5.60	0.72	0.05	133.7	1.74	0.72	30.17	1.02	0.09	42.60	1.01	0.02	149.8	0.96	-1.62
16.	RLM 185	5.40	2.42**	-0.01	119.9	0.05	17.40	22.10	3.36	-0.12	42.10	2.10*	-0.08	161.2	0.56	-0.63
17.	Durga mani	4.80	1.65	0.00	131.4	0.72	-0.03	27.40	0.98	0.03	39.60	0.49	0.37	158.9	0.17	0.43
18.	Pusa Bold	5.60	1.52	0.56	136.1	1.10	6.10	32.80	0.96	0.07	42.10	1.16	0.31	172.6	1.05	0.01
19.	Rohini	5.00	1.61	0.03	132.8	1.54	8.45	21.85	0.67	0.41	40.00	0.89	2.20**	162.2	0.97	4.21
20.	Maya	4.90	2.03**	0.02	130.2	0.50	0.83	23.59	-1.60	0.53	41.10	0.65	4.67**	139.7	1.16	0.02
21.	Vaibhav	4.75	0.41	-0.03	132.3	3.32	3.62	20.06	0.97	0.06	42.40	1.02	0.01	149.3	0.98	5.21
22.	Urvashi	4.80	1.91	0.07	129.8	1.83	2.80	31.69	1.02	0.10	38.60	0.36	0.49	152.2	0.57	0.42
23.	Pusa Bahar	5.40	0.96	0.38	127.4	1.50	8.32	28.70	0.98	0.03	39.45	0.98	2.60**	141.8	0.54	-1.73
24.	Pusa Jaikisan	5.2	0.52	0.15	135.0	0.06	16.36	24.96	0.91	0.12	42.50	1.10	1.07	169.3	0.73	4.10
25.	Vardan	5.50	0.94	0.01	130.4	-0.36	6.23	26.30	0.97	0.03	40.77	0.97	0.02	164.8	1.08	0.08
Population mean		4.33			124.20			26.61			40.53			153.34		
SEm ±		0.21	0.53		1.50	1.49		0.29	0.32		0.17	0.79		2.46	0.21	

Table-4 Estimates of regression coefficient values for stability parameters as per Freeman and Perkins model, (1971)

S. No.	Variety	Days to flower	No.of primary branches/plant	No.of sec. branches/plant	Height of plant (cm)	Length of main fruiting branch (cm)	No.of siliquae on main fruiting branch	1000-seed wt. (g)	Days to maturity	Yield/plant (g)	Oil content %
1.	Varuna	1.61	0.37	0.15	0.82	0.18	0.37	0.13	0.17*	0.10*	0.47*
2.	RH 819	0.80	0.12	0.18	1.15	0.14	0.24	0.19	0.19*	0.05*	0.29*
3.	Krishna	1.15	1.09	1.08	1.20	0.88	1.57	0.69	0.84*	0.91*	1.06*
4.	NDR 850	0.98	1.07	1.17	0.62	0.84	1.32	0.92	0.95*	0.84	1.08*
5.	Basanti	0.89	1.15	1.13	0.93	0.75	1.26	0.72	0.92*	0.76*	0.92*
6.	RN 393	1.34	1.24	1.21	0.63	0.85	1.20	0.74	0.98*	0.74*	0.90*
7.	Pusa Basanti	1.10	1.15	1.17	1.26	0.89	1.31	0.79	1.02*	0.77*	1.02*
8.	RH 30	1.52	1.29	1.07	1.01	0.72	1.21	0.82	0.94	0.89	1.31*
9.	Kranti	1.26	0.99	1.08	1.57	0.86	1.54	0.96	0.98	0.74*	1.44*
10.	Sej 2	0.97	1.12	1.15	1.42	0.84	1.58	0.81	1.00*	.91*	1.29*
11.	Seeta	0.91	1.30	1.21	0.80	0.97	1.73	0.77	1.03*	1.07*	1.74*
12.	RLM 198	1.10	0.96	1.30	0.89	0.83	1.34	0.95	0.99*	0.96*	1.08*
13.	Pusa Jagnnath	0.78	1.10	1.22	0.78	0.94	1.44	0.76	1.09*	0.93*	0.96*
14.	RH 9304	0.91	1.12	1.19	0.87	1.01	1.46	0.87	0.97*	0.89	0.92*
15.	Jawahar 1	1.60	1.05	1.21	0.72	1.19	1.26	0.86	0.91*	1.04*	0.87*
16.	RLM 185	1.47	1.06	1.08	0.52	0.87	1.51	0.92	1.02*	0.90*	1.31*
17.	Durga mani	0.88	1.18	1.09	0.10	0.77	1.31	0.64	1.11*	0.94*	1.42*
18.	Pusa Bold	0.79	1.11	1.17	1.00	0.93	1.42	0.73	0.92	0.80*	1.06*
19.	Rohini	0.92	0.94	1.14	0.94	1.02	1.26	0.76	0.94	0.98*	1.20*
20.	Maya	0.96	0.91	1.31	1.18	0.94	1.37	0.90	0.96*	0.84*	1.21*
21.	Vaibhav	0.71	1.07	1.14	0.99	1.05	1.28	0.81	0.88*	1.07*	0.99*
22.	Urvashi	1.36	1.01	1.26	0.52	0.81	1.22	0.78	1.12*	0.79*	0.37*
23.	Pusa Bahar	1.11	0.97	1.21	0.49	0.77	1.49	0.94	1.02*	1.03*	1.10*
24.	Pusa Jaikisan	1.07	0.90	1.14	0.62	0.76	1.25	0.87	0.85*	0.98*	1.01*
25.	Vardan	1.36	1.08	1.09	1.03	0.97	1.82	0.85	0.96*	0.76*	1.72*
Population mean											
SEm ±											

Table5- Analysis of variance for stability parameters according to Finlay, and Wilkinson model, 1963.

Source of variation	Degree of freedom	Days to flower	No. of primary branches/plant	No. of secondary branches/plant	Height of plant (cm)	Length of main fruiting branch	No. of Siliquae or Main fruiting branch	1000-seed weight (g)	Days to maturity	Yield/plant (g)	Oil Content
Genotypes	24	27.28**	8.25**	6.25**	70.85**	206.10**	194.60**	0.65**	66.71**	8.93**	5.15**
Environments	23	673.68**	4.95**	24.34**	4542.24**	5022.23**	5716.33**	0.64**	59.20**	262.76**	11.95**
GxE	552	18.77**	11.40**	4.63**	268.44**	45.94**	53.22**	0.69**	16.52**	9.87**	3.41**
Regressions	24	17.35**	9.86**	3.67**	279.85**	51.47**	44.75**	0.39**	32.76**	4.45**	0.55*
Deviations from regression	528	40.47**	4.16**	2.72**	39.84*	40.33**	51.43**	0.20**	6.75**	3.59**	0.91*
Residual	1152	0.59	1.43	0.62	20.32	10.81	4.92	0.06	0.72	1.16	0.54

*** significant at p = 0.05**

**** significant at p = 0.01**

Table-6: Estimates of stability parameters for seed yield and its components in Indian mustard as per Finlay and Wilkinson model (1963).

S. No.	Variety	Days to flower		Primary branches/plant		Sec. branches/plant		Length of main fruiting branch		Seliquae on main fruity branch	
		×	bi	×	bi	×	bi	×	bi	×	bi
26.	Varuna	45.20	0.96	7.20	2.19	13.30	1.12	0.20	0.91	48.52	0.87
27.	RH 819	44.53	1.62	7.00	-0.16	11.20	0.69	67.60	1.03	46.43	1.09
28.	Krishna	44.84	0.89	7.47	2.45	9.60	1.19	69.90	1.21	48.10	0.89
29.	NDR 850	43.70	0.99	6.00	4.08	11.90	1.07	71.10	1.10	49.80	0.94
30.	Basanti	44.30	0.87	5.40	1.89	8.33	1.32	76.80	0.94	46.20	0.82
31.	RN 393	46.73	1.26	6.57	2.09	12.10	0.94	79.40	0.87	46.50	1.17
32.	Pusa Basanti	44.15	1.17	5.27	-0.35	11.00	4.05	68.62	1.23	44.06	1.06
33.	RH 30	46.36	0.77	7.17	0.67	9.20	1.53	74.35	0.05	48.64	0.72
34.	Kranti	44.50	1.53	7.63	0.56	11.30	1.07	81.62	1.20	43.20	1.38
35.	Sej 2	46.16	1.21	8.33	0.89	12.80	0.79	81.95	1.22	46.60	1.26
36.	Seeta	47.08	1.24	6.33	1.63	10.00	1.24	56.60	0.06	48.45	1.37
37.	RLM 198	44.20	1.16	5.37	-0.75	10.50	0.10	69.90	1.10	45.60	1.16
38.	Pusa Jagnnath	46.18	1.07	6.20	0.67	9.60	0.59	68.80	0.394	43.44	1.13
39.	RH 9304	45.90	0.54	7.42	-2.21	12.80	0.98	69.40	0.37	47.00	1.11
40.	Jawahar 1	45.20	0.66	6.80	1.74	10.33	1.02	67.77	2.19	43.67	0.69
41.	RLM 185	46.17	1.26	7.33	3.39	11.95	1.35	60.10	1.97	46.10	0.72
42.	Durga mani	45.40	0.87	7.67	0.97	9.72	0.72	74.00	0.47	43.54	1.21
43.	Pusa Bold	44.80	0.80	5.57	0.56	12.85	1.06	79.66	0.36	42.80	0.86
44.	Rohini	41.90	0.96	6.90	0.97	11.60	1.57	68.80	0.91	47.63	0.92
45.	Maya	44.20	1.20	4.55	3.047	10.756	1.21	79.40	1.80	46.80	0.98
46.	Vaibhav	43.80	0.99	6.70	1.03	10.22	0.65	76.82	1.06	48.49	0.97
47.	Urvashi	42.60	0.74	5.90	1.40	7.98	1.02	83.66	0.06	47.25	1.46
48.	Pusa Bahar	44.10	1.24	5.20	0.68	8.60	2.13	61.90	1.35	46.33	1.10
49.	Pusa Jaikisan	40.20	0.74	7.00	1.02	12.26	1.01	83.40	0.94	48.30	0.79
50.	Vardan	43.00	0.98	6.97	0.27	13.00	0.36	69.20	0.98	44.50	0.23
Population mean		44.20		6.20		10.20		68.20		45.27	
SEm ±		1.25	0.25	0.31	0.16	0.61	0.45	0.89		1.27	0.21

Contd..6..

Table-6 Contd...

S.No.	Variety	1000-seed weight (g)		Days to maturity		Yield/plant (g)		Oil content %		Height of plant (cm)	
		×	bi	×	bi	×	bi	×	bi	×	bi
26.	Varuna	6.90	1.73	130.4	3.81	27.60	2.23	41.20	0.98	141.2	0.89
27.	RH 819	4.90	0.89	134.9	1.21	29.76	0.10	42.10	1.01	144.6	1.05
28.	Krishna	5.20	0.86	130.6	1.92	30.01	2.46	40.20	0.15	154.7	1.20
29.	NDR 850	4.85	0.88	127.5	1.16	27.18	3.90	39.00	0.95	146.8	0.62
30.	Basanti	4.25	0.45	128.0	0.96	30.25	1.03	39.60	-0.36	154.2	0.93
31.	RN 393	4.73	0.49	134.6	0.50	30.54	2.10	40.40	0.37**	152.3	0.63
32.	Pusa Basanti	4.65	0.56	131.7	1.07	28.42	-0.35	40.00	-0.54	161.4	1.06
33.	RH 30	4.95	-0.09	137.2	2.42	26.32	0.63	38.60	0.90	152.7	1.01
34.	Kranti	6.10	1.25	122.6	-1.10	22.05	0.59	38.45	1.01	160.3	1.52
35.	Sej 2	5.90	0.45	126.8	0.85	20.35	0.92	40.20	0.98	172.2	1.10
36.	Seeta	4.72	-0.21	125.4	1.10	27.72	1.60	42.90	1.12	159.6	0.82
37.	RLM 198	4.98	1.24	122.7	1.55	23.38	-*0.70	40.42	0.48	130.4	0.98
38.	Pusa Jagnnath	4.83	0.26	130.2	-1.64	28.75	0.63	42.50	1.34	136.9	0.82
39.	RH 9304	5.20	0.27	132.6	0.41	25.33	-2.15	43.47	-0.59	144.3	0.87
40.	Jawahar 1	5.60	0.72	133.7	1.74	30.17	1.02	42.60	1.01	149.8	0.96
41.	RLM 185	5.40	2.42**	119.9	0.05	22.10	3.36	42.10	2.10*	161.2	0.56
42.	Durga mani	4.80	1.65	131.4	0.72	27.40	0.98	39.60	0.49	158.9	0.17
43.	Pusa Bold	5.60	1.52	136.1	1.10	32.80	0.96	42.10	1.16	172.6	1.05
44.	Rohini	5.00	1.61	132.8	1.54	21.85	0.67	40.00	0.89	162.2	0.97
45.	Maya	4.90	2.03**	130.2	0.50	23.59	-1.60	41.10	0.65	139.7	1.16
46.	Vaibhav	4.75	0.41	132.3	3.32	20.06	0.97	42.40	1.02	149.3	0.98
47.	Urvashi	4.80	1.91	129.8	1.83	31.69	1.02	38.60	0.36	152.2	0.57
48.	Pusa Bahar	5.40	0.96	127.4	1.50	28.70	0.98	39.45	0.98	141.8	0.54
49.	Pusa Jaikisan	5.2	0.52	135.0	0.06	24.96	0.91	42.50	1.10	169.3	0.73
50.	Vardan	5.50	0.94	130.4	-0.36	26.30	0.97	40.77	0.97	164.8	1.08
Population mean		4.33		124.20		26.61		40.53		153.34	
SEm ±		0.21	0.53	1.50	1.49	0.29	0.32	0.17	0.79	2.46	0.21

Table – 7 : Genotypic and phenotypic correlation coefficient in Indian mustard (pooled over environment)

Character	Plant height (cm)	Length of main reaceme	Number of primary branches	Number of secondary branches	Days to 50% flower	No. of siliquae on main raceme	Days to maturity	1000 seed weight (g)	Oil content (%)	Seed yield /plant (g)
Plant height	X r_g r_p	0.634** (0.621)**	0.251* (0.196)	0.134 (0.104)	-0.224 (-0.179)	0.157 (0.115)	-0.045 (-0.034)	0.161 (0.126)	-0.231 (-0.132)	0.155 (0.143)
Length of main raceme		X r_g r_p	0.041 (0.060)	0.157 (0.123)	-0.284** (-0.216)	0.229* (0.190)	-0.075 (-0.021)	0.164 (0.128)	-0.289** (-0.183)	0.106 (0.107)
Number of primary branches			X r_g r_p	-0.025 (0.050)	0.001 (-0.034)	-0.190 (-0.034)	-0.197 (-0.092)	0.033 (0.004)	0.153 (0.167)	0.843** (0.549)**
Number of secondary branches				X r_g r_p	-0.417** (-0.309)	0.141 (0.060)	-0.178 (-0.143)	0.003 (0.014)	0.502** (0.313)**	0.290** (0.263)*
Days to 50% flower					X r_g r_p	-0.547** (-0.464)**	0.375** (0.344)**	0.041 (-0.003)	-0.230* (-0.156)	-0.193 (-0.158)
No. of siliquae on main raceme						X r_g r_p	0.544** (0.644)**	-0.475** (-0.339)**	0.050 (-0.028)	-0.087 (-0.061)
Days to maturity							X r_g r_p	-0.575** (-0.442)**	-0.212 (-0.168)	-0.360** (-0.263)**
Seed weight (g)								X r_g r_p	0.254** (0.177)	0.396** (0.364)**
Oil content (%)									X r_g r_p	0.416** (0.280)**
seed yield/ plant										X r_g r_p

* Significant at p=0.05, ** Significant at p=0.01.

Table-8 : Direct (diagonal) and indirect effect for yield components in Indian mustard (pooled over environments)

Character	Plant height (cm)	Length of main reaceme	Number of primary branches	Number of secondary branches	Days to 50% flower	No. of siliquae on main raceme	Days to maturity	1000 seed weight (g)	Oil content (%)	Genotypic correlation with yield
	X_1	X_2	X_{13}	X_4	X_5	X_6	X_7	X_8	X_9	
Plant height (cm)	**-0.347**	-0.211	0.290	0.114	-0.473	0.437	0.094	0.107	0.144	0.155
Length of main reaceme	-0.220	**-0.333**	0.048	0.134	-0.602	0.635	0.155	0.109	0.181	0.106
Number of primary branches	-0.087	-0.014	**1.156**	-0.021	0.002	-0.529	0.409	0.022	-0.095	0.843**
Number of secondary branches	-0.046	-0.052	-0.029	**0.851**	-0.883	0.392	0.369	0.002	-0.313	0.290**
Days to 50% flower	0.078	0.095	0.001	-0.355	**2.117**	-1.521	-0.779	0.028	0.144	-0.193
No. of siliquae on main raceme	-0.055	-0.076	-0.220	0.120	-1.159	**2.779**	-1.128	-0.316	-0.031	-0.087
Days to maturity	0.016	0.025	-0.228	-0.151	0.794	1.511	**-2.075**	-0.383	0.133	0.360
1000 seed weight (g)	-0.056	-0.055	0.038	0.003	0.088	-1.320	1.193	**0.666**	-0.159	0.398**
Oil content (%)	0.080	0.096	0.177	0.427	-0.488	0.139	0.440	0.169	**-0.625**	0.416**

Bold values showed direct effects. **Resedual effect = 0.231**

Table-9 : Estimates of phenotypic, genotypic coefficient of variability heritability and genetic advance on pooled basis in Indian mustard.

Character	Coefficient of variation (%)		Heritability	Genetic advance (K=2.06)	G.A. over mean (%)
	PCV	GCV	(b.s.)		
1. Days to flower	11.10	9.73	76.90	7.63	17.57
2. No. of primary branches/plant	20.92	12.61	36.30	0.80	15.68
3. No. of secondary branches/plant	21.00	18.00	74.80	5.67	32.34
4. Height of the plant (cm)	8.49	8.7	90.27	29.40	15.80
5. Length of main raceme	17.00	15.97	88.31	23.65	30.90
6. Siliquae on main raceme	6.10	4.93	58.89	6.80	7.81
7.1000-seed weight (g)	26.10	23.40	81.00	1.50	43.30
8. Days to maturity	4.50	3.50	61.20	7.38	5.67
9. Yield per plant (g)	38.90	37.96	95.29	14.60	76.40
10. Oil content (%)	4.75	3.16	44.40	1.70	4.31

Appendix

STATE-WISE AREA, PRODUCTION AND YIELD OF RAPESEED AND MUSTARD(1997-98)						
STATE	AREA (M.HECTS)	% OF TOTAL AREA	PRODUCTION (M.TONNES)	% OF TOTAL PRODUCTION	YIELD (KGS/HECT)	% COVERAGE UNDER IRRIGATION (1995-96)
1	2	3	4	5	6	12
ASSAM	0.28	4	0.15	3.2	554	-
BIHAR	0.1	1.4	0.09	1.9	887	33.3
GUJARAT	0.35	5	0.35	7.4	1013	97.8
HARYANA	0.56	7.9	0.37	7.9	667	66.8
MADHYA PRADESH	0.74	10.5	0.42	8.9	574	45.3
PUNJAB	0.07	1	0.06	1.3	871	87.4
RAJASTHAN	3.28	46.5	2.19	46.5	670	73.4
UTTAR PRADESH	1.2	17	0.71	15.1	593	75.2
WEST BENGAL	0.33	4.7	0.25	5.3	767	85.2
OTHERS	0.15	2.1	0.12	2.5	.	.
ALL-INDIA	7.06	100	4.71	100	667	66.3